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 ENDDOC-1203445 **PCT**  
 FILE-U.S. PATENTS 22300.28001.00  
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INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification <sup>5</sup> : C12N 15/86, 7/01, A61K 39/12	A1	(11) International Publication Number: WO 92/10578 (43) International Publication Date: 25 June 1992 (25.06.92)
(21) International Application Number: PCT/SE91/00855 (22) International Filing Date: 12 December 1991 (12.12.91) (30) Priority data: 9003978-5 13 December 1990 (13.12.90) SE (71) Applicant (for all designated States except US): BIOPTION AB [SE/SE]; Elgentorpsvägen 16 II, S-146 30 Tullinge (SE). (72) Inventors; and (75) Inventors/Applicants (for US only): GAROFF, Henrik [SE/SE]; Kroppåsbacken, S-126 58 Hägersten (SE). LILJESTRÖM, Peter [SE/SE]; Elgentorpsvägen 16, S-146 00 Tullinge (SE). (74) Agent: AB STOCKHOLMS PATENTBYRÅ; Zacco & Bruhn, P.O. Box 23101, S-104 35 Stockholm (SE).		(81) Designated States: AT, AT (European patent), AU, BB, BE (European patent), BF (OAPI patent), BG, BJ (OAPI patent), BR, CA, CF (OAPI patent), CG (OAPI patent), CH, CH (European patent), CI (OAPI patent), CM (OAPI patent), DE, DE (European patent), DK, DK (European patent), ES, ES (European patent), FI, FR (European patent), GA (OAPI patent), GB, GB (European patent), GN (OAPI patent), GR (European patent), HU, IT (European patent), JP, KP, KR, LK, LU, LU (European patent), MC (European patent), MG, ML (OAPI patent), MR (OAPI patent), MW, NL, NL (European patent), NO, PL, RO, SD, SE, SE (European patent), SN (OAPI patent), SU*, TD (OAPI patent), TG (OAPI patent), US.  Published With international search report.

(54) Title: DNA EXPRESSION SYSTEMS BASED ON ALPHAVIRUSES

(57) Abstract

Efficient protein production from cloned DNA in animal cells has been hampered by the lack of suitable expression systems. The requirements of such an expression system are (1) to produce functional or immunogenic forms of protein molecules in a wide variety of animal cells, (2) high efficiency and (3) technical simplicity. The present invention is related to a technical solution to this problem. A DNA molecule encoding protein sequences is inserted into engineered variants of the cDNA of a positive stranded RNA virus genome from alphavirus which then, via RNA transcription and transfection into tissue culture cells, is used to produce either chimaeric virus particles for immunization or recombinant virus for protein production. Because of optimized conditions of transfection and the nature of the virus replication the present system combines both simplicity and safety in terms of handling, efficiency in terms of level of protein and RNA production, as well as broad host range.

# + DESIGNATIONS OF "SU"

Any designation of "SU" has effect in the Russian Federation. It is not yet known whether any such designation has effect in other States of the former Soviet Union.

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cells of mammalian origin in order for them to become active, this system cannot be used in such cases. Furthermore, the Baculovirus cDNA expression system is not practically convenient for analysis of the relationship between structure and function of a protein because this involves in general the analysis of whole series of mutant variants. Today it takes about 6-8 weeks to construct a single Baculo recombinant virus for phenotype analyses. This latter problem is also true for the rather efficient Vaccinia recombinant virus and other contemporary recombinant virus cDNA expression systems (2,3). The procedure to establish stably transformed cell lines is also a very laborious procedure, and in addition, often combined with very low levels of protein expression.

Hitherto, most attempts to develop viral DNA expression systems have been based on viruses having DNA genomes or retroviruses, the replicative intermediate of the latter being double stranded DNA.

Recently, however, also viruses comprising RNA genomes have been used to develop DNA expression systems.

In EP 0 194 809 RNA transformation vectors derived from (+) strand RNA viruses are disclosed which comprise capped viral RNA that has been modified by insertion of exogenous RNA into a region non-essential for replication of said virus RNA genome. These vectors are used for expression of the function of said exogenous RNA in cells transformed therewith. The RNA can be used in solution or packaged into capsids. Furthermore, this RNA can be used to generate new cells having new functions, i.e. protein expression. The invention of said reference is generally claimed as regards host cells, (+) strand RNA viruses and the like. Nevertheless, it is obvious from the experimental support provided therein that only plant cells have been transformed and in addition only Bromo Mosaic virus, a plant

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member of the Alphavirus genus, the Sindbis virus, can tolerate insertion and direct the expression of at least one foreign gene, the bacterial chloramphenicol acetyl transferase (CAT) gene, it is evident from the results described that both systems described above are both ineffective in terms of exogenous gene expression and also very cumbersome to use. Hence, neither system has found any usage in the field of DNA expression in animal cells today.

In the first example a cDNA copy of a defective interfering (DI) virus variant of Sindbis virus was used to carry the CAT gene. RNA was transcribed in vitro and used to transfect avian cells and some CAT protein production could be demonstrated after infecting cells with wild-type Sindbis virus. The latter virus provided the viral replicase for expression of the CAT construct. The inefficiency of this system depends on 1) low level of initial DI-CAT RNA transfection (0.05-0.5 % of cells) and 2) inefficient usage of the DI-CAT RNA for protein translation because of unnatural and suboptimal protein initiation translation signals. This same system also results in packaging of some of the recombinant DI-CAT genomes into virus particles. However, this occurs simultaneously with a very large excess of wild-type Sindbis virus production. Therefore, the usage of this mixed virus stock for CAT expression will be much hampered by the fact that most of the replication and translation activity of the cells infected with such a stock will deal with the wild-type and not with recombinant gene expression.

Much of the same problems are inherent to the other Sindbis expression system described. In this an RNA replication competent Sindbis DNA vector is used to carry the CAT gene. RNA produced in vitro is shown to replicate in animal cells and CAT activity is found. However, as only a very low number of cells are transfected the overall CAT production remains low. Another



possible explanation for this is that the Sindbis construct used is not optimal for replication. Wild-type Sindbis virus can be used to rescue the recombinant genome into particles together with an excess of wild-type genomes and this mixed stock can then be used to express a CAT protein via infection. However, this stock has the same problems as described above for the recombinant DI system. The latter paper shows also that if virus is amplified by several passages increased titres of the recombinant virus particles can be obtained. However, one should remember that the titre of the wild-type virus will increase correspondingly and the original problem of mostly wild-type virus production remains. There are also several potential problems when using several passages to produce a mixed virus stock. As there is no selected pressure for preservation of the recombinant genomes these might easily 1) undergo rearrangements and 2) become outnumbered by wild-type genomes as a consequence of less efficient replication and/or packaging properties.

Another important aspect of viral DNA expression vectors is use thereof to express antigens of unrelated pathogens and thus they can be used as vaccines against such pathogens.

Development of safe and effective vaccines against viral diseases has proven to be quite a difficult task. Although many existing vaccines have helped to combat the worldwide spread of many infectious diseases, there is still a large number of infectious agents against which effective vaccines are missing. The current procedures of preparing vaccines present several problems: (1) it is often difficult to prepare sufficiently large amounts of antigenic material; (2) In many cases there is the additional hazard that the vaccine preparation is not killed or sufficiently attenuated; (3) Effective vaccines are often hard to produce since there is a major difficulty in presenting the antigenic epitope in

an immunologically active form; (4) In the case of many viruses, genetic variations in the antigenic components results in the evolution of new strains with new serological specificities, which again creates a need for the development of new vaccines.

Two types of viral DNA vectors have been developed in order to overcome many of these problems in vaccine production. These either provide recombinant viruses or provide chimaeric viruses. The recombinant viruses contain a wild-type virus package around a recombinant genome. These particles can be used to infect cells which then produce the antigenic protein from the recombinant genome. The chimaeric viruses also contain a recombinant genome but this specifies the production of an antigen, usually as part of a normal virus structural protein, which then will be packaged in progeny particles and e.g. exposed on the surface of the viral spike proteins. The major advantages of these kind of virus preparations for the purpose of being used as a vaccine are 1) that they can be produced in large scale and 2) that they provide antigen in a natural form to the immunological system of the organism. Cells, which have been infected with recombinant viruses, will synthesize the exogenous antigen product, process it into peptides that then present them to T cells in the normal way. In the case of the chimaeric virus there is, in addition, an exposition of the antigen in the context of the subunits of the virus particle itself. Therefore, the chimaeric virus is also called an epitope carrier.

The major difficulty with these kind of vaccine preparations are, how to ensure a safe and limited replication of the particles in the host without side effects. So far, some success has been obtained with vaccinia virus as an example of the recombinant virus approach (69) and of polio virus as an example of a chimaeric particle (70-72). As both virus variants are

based on commonly used vaccine strains one might argue that they could be useful vaccine candidates also as recombinant respectively chimaeric particles (69-72). However, both virus vaccines are combined with the risk for side effects, even severe ones, and in addition these virus strains have already been used as vaccines in large parts of the population in many countries.

As is clear from the afore mentioned discussion there is much need to develop improved DNA expression systems both for an easy production of important proteins or polypeptides in high yields in various kinds of animal cells and for the production of recombinant viruses or chimaeric viruses to be used as safe and efficient vaccines against various pathogenes.

Thus, an object of the present invention is to provide an improved DNA expression system based on virus vectors which can be used both to produce proteins and polypeptides and as recombinant virus or chimaeric virus, which system offers many advantages over prior art.

To that end, according to the present invention there is provided an RNA molecule derived from an alphavirus RNA genome and capable of efficient infection of animal host cells, which RNA molecule comprises the complete alphavirus RNA genome regions, which are essential to replication of the said alphavirus RNA, and further comprises an exogenous RNA sequence capable of expressing its function in said host cell, said exogenous RNA sequence being inserted into a region of the RNA molecule which is non-essential to replication thereof.

Alphavirus is a genus belonging to the family Togaviridae having single stranded RNA genomes of positive polarity enclosed in a nucleocapsid surrounded by an envelope containing viral spike proteins.

The Alphavirus genus comprises among others the Sindbis virus, the Semliki Forest virus (SFV) and the Ross River virus, which are all closely related.

According to a preferred embodiment of the invention, the Semliki Forest virus (SFV) is used as the basis of the DNA expression system.

5 The exogenous RNA sequence encodes a desired genetic trait, which is to be conferred on the virus or the host cell, and said sequence is usually complementary to a DNA or cDNA sequence encoding said genetic trait. Said DNA sequence may be comprised of an isolated natural gene, such as a bacterial or mammalian gene, or  
10 may constitute a synthetic DNA sequence coding for the desired genetic trait i.e. expression of a desired product, such as an enzyme, hormone, etc. or expression of a peptide sequence defining an exogenous antigenic epitope or determinant.

15 If the exogenous RNA sequence codes for a product, such as a protein or polypeptide, it is inserted into the viral RNA genome replacing deleted structural protein encoding region(s) thereof, whereas a viral epitope encoding RNA sequence may be inserted into  
20 structural protein encoding regions of the viral RNA genome, which essentially do not comprise deletions or only have a few nucleosides deleted.

The RNA molecule can be used per se, e.g. in solution to transform animal cells by conventional transfection, e.g. the DEAE-Dextran method or the calcium phosphate  
25 precipitation method. However, the rate of transformation of cells, and, thus the expression rate can be expected to increase substantially if the cells are transformed by infection with infectious viral particles. Thus, a suitable embodiment of the invention is  
30 related to an RNA virus expression vector comprising the RNA molecule of this invention packaged into infectious particles comprising the said RNA within the alphavirus nucleocapsid and surrounded by the membrane including the alphavirus spike proteins.  
35

The RNA molecule of the present invention can be packaged into such particles without restraints pro-

vided that it has a total size corresponding to the wild type alphavirus RNA genome or deviating therefrom to an extent compatible with package of the said RNA into the said infectious particles.

5        These infectious particles, which include recombinant genomes packaged to produce a pure, high titre recombinant virus stock, provides a means for exogenous genes or DNA sequences to be expressed by normal virus particle infection, which as regards transformation degree, is much more efficient than RNA transfection.

10        According to a suitable embodiment of the invention such infectious particles are produced by cotransfection of animal host cells with the present RNA which lacks part of or the complete region(s) encoding the structural viral proteins together with a helper RNA molecule transcribed in vitro from a helper DNA vector comprising the SP6 promoter region, those 5' and 3' regions of the alphavirus cDNA which encode cis acting signals needed for RNA replication and the region encoding the viral structural proteins but lacking essentially all of the nonstructural virus proteins encoding regions including sequences encoding RNA signals for packaging of RNA into nucleocapsid particles, and culturing the host cells.

25        According to another aspect of the invention efficient introduction of the present RNA into animal host cells can be achieved by electroporation. For example, in the case of Baby Hamster Kidney (BHK) cells a transformation degree of almost 100 % has been obtained for the introduction of an RNA transcript derived from SFV cDNA of the present invention. This makes it possible to reach so high levels of exogenous protein production in every cell that the proteins can be followed in total cell lysates without the need of prior concentration by antibody precipitation.

35        By electroporation, it is also possible to obtain a high degree of cotransfection in the above process for

production of infectious particles comprising packaged RNA of the present invention. Essentially all animal cells will contain both the present RNA molecule and the helper RNA molecule, which leads to a very efficient trans complementation and formation of infectious particles. A pure recombinant virus stock, consisting of up to  $10^9$ - $10^{10}$  infectious particles, can be obtained from  $5 \times 10^6$  cotransfected cells after only a 24 h incubation. Furthermore, the so obtained virus stock is very safe to use, since it is comprised of viruses containing only the desired recombinant genome, which can infect host cells but can not produce new progeny virus.

Theoretically, a regeneration of a wild-type virus genome could take place when producing the recombinant virus in the cotransfected cells. However, the possibility to avoid spread of such virus can be eliminated by incorporating a conditionally lethal mutation into the structural part of the helper genome. Such a mutation is described in the experimental part of this application. Thus, the virus produced with such a helper will be noninfectious if not treated in vitro under special conditions.

The technique of electroporation is well known within the field of biotechnology and optimal conditions can be established by the man skilled in the art. For instance, a BioRad Gene pulser apparatus (BioRad, Richmond, CA, USA) can be used to perform said process.

The RNA molecule of the present invention is derived by in vivo or in vitro transcription of a cDNA clone, originally produced from an alphavirus RNA and comprising an inserted exogenous DNA fragment encoding a desired genetic trait.

Accordingly, the present invention is also related to a DNA expression vector comprising a full-length or partial cDNA complementary to alphavirus RNA or parts thereof and located immediately downstream of the SP6

RNA polymerase promoter and having a 5'ATGG, a 5'GATGG or any other 5' terminus and a TTTCCA<sub>69</sub>ACTAGT or any other 3' terminus.

5 According to one aspect of the present invention portions of the viral cDNA are deleted, the deletions comprising the complete or part of the region(s) encoding the virus structural proteins, and the vector further comprises an integrated polylinker region, which may correspond to BamHI-SmaI-XmaI, inserted at a  
10 location which enables an exogenous DNA fragment encoding a foreign polypeptide or protein to be inserted into the vector cDNA for subsequent expression in an animal host cell.

15 According to another aspect of this invention, the vector is comprised of full-length cDNA wherein an exogenous DNA fragment encoding a foreign epitopic peptide sequence can be inserted into a region coding for the viral structural proteins.

20 It is appreciated that this cDNA clone with its exogenous DNA insert is very efficiently replicated after having been introduced into animal cells by transfection.

25 A very important aspect of the present invention is that it is applicable to a broad range of host cells of animal origin. These host cells can be selected from avian, mammalian, reptilian, amphibian, insect and fish cells. Illustrative of mammalian cells are human, monkey, hamster, mouse and porcine cells. Suitable avian cells are chicken cells, and as reptilian cells  
30 viper cells can be used. Cells from frogs and from mosquitoes and flies (*Drosophila*) are illustrative of amphibian and insecticidal cells, respectively. A very efficient virus vector/host cell system according to the invention is based on SFV/BHK cells, which will be  
35 discussed more in detail further below.

However, even though a very important advantage of the present DNA expression vector is that it is very

efficient in a broad variety of animal cells it can also be used in other eucaryotic cells and in pro-caryotic cells.

5 The present invention is also related to a method to produce transformed animal host cells comprising transfection of the cells with the present RNA molecule or with the present transcription vector comprised of cDNA and carrying an exogenous DNA fragment. According to a  
10 suitable embodiment of the invention, transfection is produced by the above mentioned electroporation method, a very high transfection rate being obtained.

A further suitable transformation process is based on infection of the animal host cells with the above  
15 mentioned infectious viral particles comprising the present RNA molecule.

The transformed cells of the present invention can be used for different purposes.

One important aspect of the invention is related to use of the present transformed cells to produce a poly-  
20 peptide or a protein by culturing the transformed cells to express the exogenous RNA and subsequent isolation and purification of the product formed by said exepression. The transformed cells can be produced by infec-  
25 tion with the present viral particles comprising exogenous RNA encoding the polypeptide or protein as mentioned above, or by transfection with an RNA transcript obtained by in vitro transcription of the present DNA vector comprised of cDNA and carrying an exogenous DNA fragment coding for the polypeptide or the protein.

30 Another important aspect of the invention is related to use of the present transformed cells for the production of antigens comprised of chimaeric virus particles for use as immunizing component in vaccines or for  
immunization purposes for in vivo production of  
35 immunizing components for antisera production.

Accordingly, the present invention is also related to an antigen consisting of a chimaeric alphavirus having



an exogenous epitopic peptide sequence inserted into its structural proteins.

Preferably, the chimaeric alphavirus is derived from SFV.

5 According to a suitable embodiment, the exogenous epitopic peptide sequence is comprised of an epitopic peptide sequence derived from a structural protein of a virus belonging to the immunodeficiency virus class inclusive of the human immunodeficiency virus types.

10 A further aspect of the invention is related to a vaccine preparation comprising the said antigen as immunizing component.

15 In said vaccine the chimaeric alphavirus is suitably attenuated by comprising mutations, such as the conditionally lethal SFV-mutation described before, amber (stop codon) or temperature sensitive mutations, in its genome.

20 For instance, if the chimaeric virus particles containing the afore mentioned conditional lethal mutation in its structural proteins (a defect to undergo a certain proteolytical cleavage in host cell during morphogenesis) is used as a vaccine then this is first activated by limited proteolytic treatment before given to the organism so that it can infect recipient cells.  
25 New chimaeric particles will be formed in cells infected with the activated virus but these will again be of the lethal phenotype and further spread of infection is not possible.

30 The invention is also concerned with a method for the production of the present antigen comprising

a) in vitro transcription of the cDNA of the present DNA vector carrying an exogenous DNA fragment encoding the foreign epitopic peptide sequence and transfection of animal host cells with the produced RNA transcript,  
35 or

b) transfection of animal host cells with the said cDNA of the above step a),

culturing the transfected cells and recovering the chimaeric alphavirus antigen. Preferably, transfection is produced by electroporation.

5 Still another aspect of the invention is to use a recombinant virus containing exogenous RNA encoding a polypeptide antigen for vaccination purpose or to produce antisera. In this case the recombinant virus or the conditionally lethal variant of it is used to infect cells in vivo and antigen production will take  
10 place in the infectious cells and used for antigen presentation to the immunological system.

According to another embodiment of the invention, the present antigen is produced in an organism by using in vivo infection with the present infectious particles  
15 containing exogenous RNA encoding an exogenous epitopic peptide sequence.

In the following, the present invention will be illustrated more in detail with reference to the Semliki Forest virus (SFV), which is representative for  
20 the alphaviruses. This description can be more fully understood in conjunction with the accompanying drawings in which:

Fig. 1 is a schematic view over the main assembly and disassembly events involved in the life cycle of the  
25 Semliki Forest virus, and also shows regulation of the activation of SFV entry functions by p62 cleavage and pH;

Fig. 2 illustrates the use of translocation signals during synthesis of the structural proteins of SFV;  
30 top, the gene map of the 26S subgenomic RNA; middle, the process of membrane translocation of the p62, 6K and E1 proteins; small arrows on the luminal side denote signal peptidase cleavages; at the bottom, the  
35 characteristics of the three signal peptides are listed;

Fig. 3 shows features that make SFV an excellent

choice as an expression vector;

5 Fig. 4 A-C show the construction of full-length infectious clones of SFV; Fig. 4A shows a schematic restriction map of the SFV genome; primers used for initiating cDNA synthesis are indicated as arrows, and the cDNA inserts used to assemble the final clone are showed as bars; Fig. 4B shows plasmid pPLH211, i.e. the SP6 expression vector used as carrier for the full-length infectious clone of SFV, and the resulting plasmid pSP6-SFV4; Fig. 4C shows the structure of the SP6 promoter area of the SFV clone; the stippled bars indicate the SP6 promoter sequence, and the first nucleotide to be transcribed is marked by an asterisk; underlined regions denote authentic SFV sequences;

10 Fig. 5 shows the complete nucleotide sequence of the pSP6-SFV4 RNA transcript as DNA (U = T) and underneath the DNA sequence, the amino acid sequence of the non-structural polyprotein and the structural polyprotein;

15 Fig. 6 shows an SFV cDNA expression system for the production of virus after transfection of in vitro made RNA into cells;

20 Fig. 7 shows the construction of the SFV expression vectors pSFV1-3 and of the Helper 1;

25 Fig. 8 shows the polylinker region of SFV vector plasmids pSFV1-3; the position of the promoter for the subgenomic 26S RNA is boxed, and the first nucleotide to be transcribed is indicated by an asterisk;

30 Fig. 9 is a schematic presentation of in vivo packaging of pSFV1-dhfr RNA into infectious particles using helper trans complementation; (dhfr means dihydrofolate reductase)

Fig. 10 shows the use of trypsin to convert p62-containing noninfectious virus particles to infectious particles by cleavage of p62 to E2 and E3;

35 Fig. 11 shows the expression of heterologous proteins in BHK cells upon RNA transfection by electroporation; and

Fig. 12 shows in its upper part sequences encompassing the major antigenic site of SFV and the in vitro made substitutions leading to a BamHI restriction endonuclease site, sequences spanning the principal neutralizing domain of the HIV gp120 protein, and the HIV domain inserted into the SFV carrier protein E2 as a BamHI oligonucleotide; and its lower part is a schematic presentation of the SFV spike structure with blow-ups of domain 246-251 in either wild type or chimaeric form.

The alphavirus Semliki Forest virus (abbreviated SFV in the following text) has for some 20 years been used as model system in both virology and cell biology to study membrane biosynthesis, membrane structure and membrane function as well as protein-RNA interactions (4, 5). The major reason for the use of SFV as such a model is due to its simple structure and efficient replication.

With reference to Fig. 1-3, in the following the SFV and its replication are explained more in detail. In essential parts, this disclosure is true also for the other alphaviruses, such as the Sindbis virus, and many of the references cited in this connection are indeed directed to the Sindbis virus. SFV consists of an RNA-containing nucleocapsid and a surrounding membrane composed of a lipid bilayer and proteins, a regularly arranged icosahedral shell of a protein called C protein forming the capsid inside which the genomic RNA is packaged. The capsid is surrounded by the lipid bilayer that contains three proteins called E1, E2, and E3. These so-called envelope proteins are glycoproteins and their glycosylated portions are on the outside of the lipid bilayer, complexes of these proteins forming the "spikes" that can be seen in electron micrographs to project outward from the surface of the virus.

The SFV genome is a single-stranded 5'-capped and 3'-polyadenylated RNA molecule of 11422 nucleotides (6,7).

It has positive polarity, i.e. it functions as an mRNA, and naked RNA is able to start an infection when introduced into the cytoplasm of a cell. Infection is initiated when the virus binds to protein receptors on the host cell plasma membrane, whereby the virions become selectively incorporated into "coated pits" on the surface of the plasma membrane, which invaginate to form coated vesicles inside the cell, whereafter said vesicles bearing endocytosed virions rapidly fuse with organelles called endosomes. From the endosome, the virus escapes into the cell cytosol as the bare nucleocapsid, the viral envelope remaining in the endosome. Thereafter, the nucleocapsid is "uncoated" and, thus, the genomic RNA is released. Referring now to Fig. 1, infection then proceeds with the translation of the 5' two-thirds of the genome into a polyprotein which by self-cleavage is processed to the four nonstructural proteins nsP1-4 (8). Protein nsP1 encodes a methyl transferase which is responsible for virus-specific capping activity as well as initiation of minus strand synthesis (9, 10); nsP2 is the protease that cleaves the polyprotein into its four subcomponents (11, 12); nsP3 is a phosphoprotein (13, 14) of as yet unknown function, and nsP4 contains the SFV RNA polymerase activity (15, 16). Once the nsP proteins have been synthesized they are responsible for the replication of the plus strand (42S) genome into full-length minus strands. These molecules then serve as templates for the production of new 42S genomic RNAs. They also serve as templates for the synthesis of subgenomic (26S) RNA. This 4073 nucleotides long RNA is colinear with the last one-third of the genome, and its synthesis is internally initiated at the 26S promoter on the 42S minus strands (17, 18).

The capsid and envelope proteins are synthesized in different compartments, and they follow separate pathways through the cytoplasm, viz. the envelope proteins

are synthesized by membrane-bound ribosomes attached to the rough endoplasmic reticulum, and the capsid protein is synthesized by free ribosomes in the cytosol. However, the 26S RNA codes for all the structural proteins of the virus, and these are synthesized as a poly-  
5 protein precursor in the order C-E3-E2-6K-E1 (19). Once the capsid (C) protein has been synthesized it folds to act as a protease cleaving itself off the nascent chain (20, 21). The synthesized C proteins bind to the re-  
10 cently replicated genomic RNA to form new nucleocapsid structures in the cell cytoplasm.

The said cleavage reveals an N-terminal signal sequence in the nascent chain which is recognized by the signal recognition particle targeting the nascent chain  
15 - ribosome complex to the endoplasmic reticulum (ER) membrane (22, 23), where it is cotranslationally translocated and cleaved by signal peptidase to the three structural membrane proteins p62 (precursor form of E3/E2), 6K and E1 (24, 25). The translocational  
20 signals used during the synthesis of the structural proteins are illustrated in Fig. 2. The membrane proteins undergo extensive posttranslational modifications within the biosynthetic transport pathway of the cell. The p62 protein forms a heterodimer with E1 via its E3  
25 domain in the endoplasmic reticulum (26). This dimer is transported out to the plasma membrane, where virus budding occurs through spike nucleocapsid interactions. At a very late (post-Golgi) stage of transport the p62  
30 protein is cleaved to E3 and E2 (27), the forms that are found in mature virions. This cleavage activates the host cell binding function of the virion as well as the membrane fusion potential of E1. The latter activity is expressed by a second, low-pH activation step  
35 after the virus enters the endosomes of a new host cell and is responsible for the release of the viral nucleocapsid into the cell cytoplasm (28-32). The mature virus particles contain one single copy of the RNA

genome encapsidated within 180 copies of the capsid protein in a T=3 symmetry, and is surrounded by a lipid bilayer carrying 240 copies of the spike trimer protein consisting of E1+E2+E3 arranged in groups of three in a T=4 symmetry (33).

The SFV entry functions are activated and regulated by p62 cleavage and pH. More specifically, the p62-E1 heterodimers formed in the ER are acid resistant. When these heterodimers are transported to the plasma membrane via the Golgi complex the E1 fusogen cannot be activated in spite of the mildly acidic environment, since activation requires dissociation of the complex. As is illustrated in Fig. 1, the released virus particles contain E2E1 complexes. Since the association between E2 and E1 is sensitive to acidic pH, during entry of the virus into a host cell through endocytosis the acidic milieu of the endosome triggers the dissociation of the spike complex (E1 E2 E3) resulting in free E1. The latter can be activated for the catalysis of the fusion process between the viral and endosomal membranes in the infection process as disclosed above.

As indicated in the preceding parts of the disclosure, the alphavirus system, and especially the SFV system, has several unique features which are to advantage in DNA expression systems. These are summarized below with reference to Fig. 3.

1. Genome of positive polarity. The SFV RNA genome is of positive polarity, i.e. it functions directly as mRNA, and infectious RNA molecules can thus be obtained by transcription from a full-length cDNA copy of the genome.

2. Efficient replication. The infecting RNA molecule codes for its own RNA replicase, which in turn drives an efficient RNA replication. Indeed, SFV is one of the most efficiently replicating viruses known. Within a few hours up to 200.000 copies of the plus-RNAs are made in a single cell. Because of the abundance of

these molecules practically all ribosomes of the infected cell will be enrolled in the synthesis of the virus encoded proteins, thus overtaking host protein synthesis (34), and pulse-labelling of infected cells results in almost exclusive labelling of viral proteins. During a normal infection  $10^5$  new virus particles are produced from one single cell, which calculates to at least  $10^8$  protein molecules encoded by the viral genome (5).

3. Cytoplasmic replication. SFV replication occurs in the cell cytoplasm, where the virus replicase transcribes and caps the subgenomes for production of the structural proteins (19). It would obviously be very valuable to include this feature in a cDNA expression system to eliminate the many problems that are encountered in the conventional "nuclear" DNA expression systems, such as mRNA splicing, limitations in transcription factors, problems with capping efficiency and mRNA transport.

4. Late onset of cytopathic effects. The cytopathic effects in the infected cells appear rather late during infection. Thus, there is an extensive time window from about 4 hours after infection to up to 24 hours after infection during which a very high expression level of the structural proteins is combined with negligible morphological change.

5. Broad host range. This phenomenon is probably a consequence of the normal life cycle which includes transmission through arthropod vectors to wild rodents and birds in nature. Under laboratory conditions, SFV infects cultured mammalian, avian, reptilian and insect cells (35) (Xiong, et al, loc. cit.)

6. In nature SFV is of very low pathogenicity for humans. In addition, the stock virus produced in tissue culture cells is apparently apathogenic. By means of specific mutations it is possible to create conditionally lethal mutations of SFV, a feature that is of



great use to uphold safety when massproduction of virus stocks is necessary.

In the nucleotide and amino acid sequences the following abbreviations have been used in this specification:

Ala, alanine; Ile, isoleucine; Leu, leucine; Met, methionine; Phe, phenylalanine; Pro, proline; Trp, tryptophan; Val, valine; Asn, asparagine; Cys, cysteine; Gln, glutamine; Gly, glycine; Ser, serine; Thr, threonine; Tys, tyrosine; Arg, arginine; His, histidine; Lys, lysine; Asp, aspartic acid; Glu, glutamic acid; A, adenine; C, cytosine; G, guanine; T, thymine; U, uracil.

The materials and the general methodology used in the following examples are disclosed below.

1. Materials. Most restriction enzymes, DNA Polymerase I, Klenow fragment, calf intestinal phosphatase, T4 DNA ligase and T4 Polynucleotide kinase were from Boehringer (Mannheim, FRG). SphI, StuI and KpnI together with RNase inhibitor (RNasin) and SP6 Polymerase were from Promega Biotec (Madison, WI). Sequenase (Modified T7 polymerase) was from United States Biochemical (Cleveland, Ohio). Proteinase K was from Merck (Darmstadt, FRG). Ribonucleotides, deoxyribonucleotides, dideoxyribonucleotides and the cap analogue m<sup>7</sup>G(5')ppp(5')G were from Pharmacia (Sweden). Oligonucleotides were produced using an Applied Biosystems synthesizer 380B followed by HPLC and NAP-5 (Pharmacia) purification. Spermidine, phenylmethylsulfonyl fluoride (PMSF), diethylpyrocarbonate (DEPC), bovine serum albumin (BSA), creatine phosphate and creatine phosphokinase were from Sigma (St. Louis, Mo). Pansorbin was from CalBiochem (La Jolla, CA). Agarose was purchased from FMC BioProducts (Rockland, Maine), and acrylamide from BioRad (Richmond, CA). L-[<sup>35</sup>S]-methionine and α-[<sup>35</sup>S]-dATP-α-S were from Amersham.

2. Virus growth and purification: BHK-21 cells were

grown in BHK medium (Gibco Life Technologies, Inc., New York) supplemented with 5 % fetal calf serum, 10 % tryptose phosphate broth, 10 mM HEPES (N-2-hydroxyethylpiperazine-N'-2-ethanesulfonic acid) and 2 mM glutamine. 90 % confluent monolayers were washed once with PBS and infected with SFV in MEM containing 0.2 % bovine serum albumin (BSA), 10 mM HEPES and 2 mM glutamine at a multiplicity of 0.1. Twenty-four hours post infection (p.i.) the medium was collected and cell debris removed by centrifugation at 8,000 xg for 20 min at 4°C. The virus was pelleted from the medium by centrifugation at 26,000 rpm for 1.5 h in an SW28 rotor at 4°C. The virus was resuspended in TN containing 0.5 mM EDTA.

3. Metabolic labeling and immunoprecipitation. Confluent monolayers of BHK cells grown in MEM supplemented with 10 mM HEPES, 2 mM glutamine, 0.2 % BSA, 100 IU/mol of penicillin and 100 µg/ml streptomycin, were infected at a multiplicity of 50 at 37°C. After 1 h p.i. the medium was replaced with fresh and growth continued for 3.5 h. The medium was removed and cells washed once with PBS and overlaid with methionine-free MEM containing 10 mM HEPES and 2 mM glutamine. After 30 min at 37°C the medium was replaced with the same containing 100 µCi/ml of [<sup>35</sup>S]methionine (Amersham) and the plates incubated for 10 min at 37°C. The cells were washed twice with labeling medium containing 10X excess methionine and then incubated in same medium for various times. The plates were put on ice, cells washed once with ice-cold PBS and finally lysis buffer (1 % NP-40 - 50 mM Tris-HCl, pH 7.6 - 150 mM NaCl - 2 mM EDTA) containing 10 µg/ml PMSF (phenylmethylsulfonyl fluoride) was added. Cells were scraped off the plates, and nuclei removed by centrifugation at 6,000 rpm for 5 min at 4°C in an Eppendorf centrifuge. Immunoprecipitations of proteins was performed as described (31). Briefly, antibody was added to lysate and the mixture

kept on ice for 30 min. Complexes were recovered by binding to Pansorbin for 30 min on ice. Complexes were washed once with low salt buffer, once with high salt buffer, and once with 10 mM Tris-HCl, pH 7.5, before heating with gel loading buffer. To precipitate dhfr, SDS was added to 0.1 % and the mixture heated to 95°C for 2 min followed by addition of 10 volumes of lysis buffer. Anti-E1 [8.139], anti-E2 [5.1] (36), and anti-C [12/2] (37) monoclonals have been described. The human transferrin receptor was precipitated with the monoclonal antibody OKT-9 in ascites fluid. This preparation was provided by Thomas Ebel at our laboratory using a corresponding hybridoma cell line obtained from ATCC (American Typ Culture Collection) No CRL 8021. Polyclonal rabbit anti-mouse dhfr was a kind gift from E. Hurt (European Molecular Biology Laboratory, Heidelberg, FRG) and rabbit anti-lysozyme has been described (38).

4. Immunofluorescence. To perform indirect immunofluorescence, infected cell monolayers on glass coverslips were rinsed twice with phosphate-buffered saline (PBS) and fixed in -20°C methanol for 6 min. After fixation, the methanol was removed and the coverslip washed 3 times with PBS. Unspecific antibody binding was blocked by incubation at room temperature with PBS containing 0.5 % gelatin and 0.25 % BSA. The blocking buffer was removed and replaced with same buffer containing primary antibody. After 30 min at room temperature the reaction was stopped by washing 3 times with PBS. Binding of secondary antibody (FITC-conjugated sheep anti-mouse [BioSys, Compiègne, France]) was done as for the primary antibody. After 3 washes with PBS and one rinse with water the coverslip was allowed to dry before mounting in Moviol 4-88 (Hoechst, Frankfurt am Main, FRG) containing 2.5 % DABCO (1,4-diazobicyclo-[2.2.2]-octane).

5. DNA procedures. Plasmids were grown in Escherichia

coli DH5 $\alpha$  (Bethesda Research Laboratories) [recA endA1 gyrA96 thi1 hsdR17 supE44 relA1  $\Delta$ (lacZYA-argF)U169  $\phi$ 80dlacZ $\Delta$ (M15)]. All basic DNA procedures were done essentially as described (39). DNA fragments were isolated from agarose gels by the freeze-thaw method (40) including 3 volumes of phenol during the freezing step to increase yield and purity. Fragments were purified by benzoyl-naphthoyl-DEAE (BND) cellulose (Serva Feinbiochemica, Heidelberg, FRG) chromatography (41). Plasmids used for production of infectious RNA were purified by sedimentation through 1 M NaCl followed by banding in CsCl (39). In some cases plasmids were purified by Qiagen chromatography (Diagen GmbH, Düsseldorf, FRG).

6. Site-directed oligonucleotide mutagenesis. For oligonucleotide mutagenesis, relevant fragments of the SFV cDNA clone were subcloned into M13mp18 or mp 19 (42) and transformed (43) into DH5 $\alpha$ FIQ [endA1 hsdR1 supE44 thi1 recA1 gyrA96 relA1  $\phi$ 80dlacZ $\Delta$ (M15)  $\Delta$ (lacZYA-argF)U169/F'proAB lacI<sup>q</sup> lacZ $\Delta$ (M15) Tn 5] (Bethesda Research Laboratories). RF DNA from these constructs was transformed into RZ1032 (44) [Hfr KL16 dut1 ung1 thi1 relA1 supE44 zbd279:Tn10.], and virus grown in the presence of uridine to incorporate uracil residues into the viral genome. Single stranded DNA was isolated by phenol extraction from PEG precipitated phage. Oligonucleotides were synthesized on an Applied Biosystems 380B synthesizer and purified by gel filtration over NAP-5 columns (Pharmacia). The oligonucleotides 5'-CGGCCAGTGAATTCTGATTGGATCCCGGGTAATTAATTGAATTACATCCCTACGCAAACG, 5'-GCGCACTATTATAGCACC GGCTCCCGGGTAATTAATTGACGCAAACGTTTACGGCCGCCCGG and 5'-GCGCACTATTATAGCACCATG-GATCCCGGGTAATTAATTGACGTTTACGGCCGCCGGTGGCG were used to insert the new linker sites [BamHI-SmaI-XmaI] into the SFV cDNA clone. The oligonucleotides 5'-CGGCGGTCCTA-GATTGGTGCG and 5'-CGCGGGCGCCACCGGCGGCCG were used as sequencing primers (SP1 and SP2) up- and downstream of

the polylinker site. Phosphorylated oligonucleotides were used in mutagenesis with Sequenase (Unites States Biochemicals, Cleveland, Ohio) as described earlier (44, 45). In vitro made RF forms were transformed into DH5 $\alpha$ F'IQ and the resulting phage isolates analyzed for the presence of correct mutations by dideoxy sequencing according to the USB protocol for using Sequenase. Finally, mutant fragments were reinserted into the full-length SFV cDNA clone. Again, the presence of the appropriate mutations was verified by sequencing from the plasmid DNA. Deletion of the 6K region has been described elsewhere.

7. In vitro transcription. SpeI linearized plasmid DNA was used as template for in vitro transcription. RNA was synthesized at 37°C for 1 h in 10-50  $\mu$ l reactions containing 40 mM Tris-HCl (pH 7.6), 6 mM spermidine-HCl, 5 mM dithiothreitol (DTT), 100  $\mu$ g/ml of nuclease free BSA, 1 mM each of ATP, CTP and UTP, 500  $\mu$ M of GTP, 1 unit/ $\mu$ l of RNasin and 100-500 units/ml of SP6 RNA polymerase. For production of capped transcripts (46), the analogs m<sup>7</sup>G(5')ppp(5')G or m<sup>7</sup>G(5')ppp(5')A were included in the reaction at 1 mM. For quantitation of RNA production, trace amounts of [ $\alpha$ -<sup>32</sup>P]-UTP (Amersham) was included in the reactions and incorporation measured from trichloroacetic acid precipitates. When required, DNA or RNA was digested at 37°C for 10 min by adding DNase 1 or RNase A at 10 units/ $\mu$ g template or 20  $\mu$ g/ml respectively.

8. RNA transfection. Transfection of BHK monolayer cells by the DEAE-Dextran method was done as described previously (47). For transfection by electroporation, RNA was added either directly from the in vitro transcription reaction or diluted with transcription buffer containing 5 mM DTT and 1 unit/ $\mu$ l of RNasin. Cells were trypsinized, washed once with complete BHK-cell medium and once with ice-cold PBS (without MgCl<sub>2</sub> and CaCl<sub>2</sub>) and finally resuspended in PBS to give 10<sup>7</sup> cells/ml. Cells

were either used directly or stored (in BHK medium) on ice over night. For electroporation, 0.5 ml of cells were transferred to a 0.2 cm cuvette (BioRad), 10-50  $\mu$ l of RNA solution added and the solution mixed by inverting the cuvette. Electroporation was performed at room temperature by two consecutive pulses at 1.5 kV/25  $\mu$ F using a BioRad Gene Pulser apparatus with its pulse controller unit set at maximum resistance. After incubation for 10 min, the cells were diluted 1:20 in complete BHK-cell medium and transferred onto tissue culture plates. For plaque assays, the electroporated cells were plated together with about  $3 \times 10^5$  fresh cells per ml and incubated at 37°C for 2 h, then overlaid with 1.8 % low melting point agarose in complete BHK-cell medium. After incubation at 37°C for 48 h, plaques were visualized by staining with neutral red.

9. Gel electrophoresis. Samples for sodium dodecyl sulfate - polyacrylamide gel electrophoresis (SDS-PAGE) were prepared and run on 12 % separating gels with a 5 % stacking gel as previously described (48). For resolving the 6K peptide, a 10 % - 20 % linear acrylamide gradient gel was used. Gels were fixed in 10 % acetic acid - 30 % methanol for 30 min before exposing to Kodak XAR-5 film. When a gel was prepared for fluorography (49), it was washed after fixation for 30 min in 30 % methanol and then soaked in 1M sodium salicylate - 30 % methanol for 30 min before drying. Nucleic acids were run on agarose gels using 50 mM Tris-borate - 2.5 mM  $\text{Na}_2\text{EDTA}$  as buffer. For staining 0.2  $\mu$ g/ml of ethidium bromide was included in the buffer and gel during the run.

#### Example 1

In this example a full-length SFV cDNA clone is prepared and placed in a plasmid containing the SP6 RNA polymerase promoter to allow in vitro transcription of full-length and infectious transcripts. This plasmid which is designated pSP6-SFV4 has been deposited on 28

NOV 1991 at PHLS Centre for Applied Microbiology & Research

European Collection of Animal Cell Cultures, Porton Down, Salisbury, Wiltshire, U.K.:, and given the provisional accession number 91112826.

As illustrated in Fig. 4A-C the strategy for construction the SFV clone was to prime cDNA synthesis on several positions along the template RNA downstream of suitable restriction endonuclease sites defined by the known nucleotide sequence of the SFV RNA molecule. Virus RNA was isolated by phenol-chloroform extraction from purified virus (obtainable among others from the Arbovirus collection in Yale University, New Haven, USA) and used as template for cDNA synthesis as previously described (50). First strand synthesis was primed at three positions, using 5'-TTTCTCGTAGTTCTCCTC-GTC as primer-1 (SFV coordinate 2042-2062) and 5'-GTTA-TCCCAGTGGTTGTTCTCGTAATA as primer-2 (SFV coordinate 3323-3349) and an oligo-dT<sub>12-18</sub> as primer -3 (3' end of SFV) Fig. 4A).

Second strand synthesis was preceded by hybridization of the oligonucleotide 5'-ATGGCGGATGTGTGACATACACGACGCC (identical to the 28 first bases of the genome sequence of SFV) to the first strand cDNA. After completion of second strand synthesis cDNA was trimmed and in all cases except in the case of the primer-1 reaction, the double-stranded adaptor 5'-AATTCAAGCTTGCGGCCGCACTAGT / GTTCGAACGCCGGCGTGATCA-3' (5'-sticky-EcoRI-HindIII-NotI-XmaIII-SpeI-blunt-3') was added and the cDNA cloned into EcoRI cleaved pTZ18R (Pharmacia, Sweden) as described (51). The cloning of the 5' end region was done in a different way. Since SFV contains a HindIII site at position 1947, cDNA primed with primer-1 should contain this area and therefore HindIII could be used to define the 3' end of that cDNA. To obtain a restriction site at the very 5' end of the SFV, cDNA was cloned into SmaI-HindIII cut pGEM1 (Promega Biotec.,

Madison, WI). Since the SFV genome starts with the sequence 5'-ATGG, ligation of this onto the blunt CCC-3' end of the SmaI site created an NcoI site C'CATGG. Although the SFV sequence contains 3 NcoI sites, none of these are within the region preceding the HindIII site, and thus these 5' end clones could be further subcloned as NcoI-HindIII fragments into a vector especially designed for this purpose (see below). The original cDNA clones in pGEM1 were screened by restriction analysis and all containing inserts bigger than 1500 bp were selected for further characterization by sequencing directly from the plasmid into both ends of the insert, using SP6 or T7 sequencing primers. The SFV 5'-end clones in pTZ18R were sequenced using lac sequencing primers. To drive in vitro synthesis of SFV RNA the SP6 promoter was used. Cloning of the SFV 5' end in front of this promoter without adding too many foreign nucleotides required that a derivative of pGEM1 had to be constructed. Hence, pGEM1 was opened at EcoRI and Bal31 deletions were created, the DNA blunted with T4 DNA polymerase and an NcoI oligonucleotide (5'-GCCATGGC) added. The clones obtained were screened by colony hybridization (39) with the oligonucleotide 5'-GGTGACACTATAGCCATGGC designed to pick up (at suitable stringency) the variants that had the NcoI sequence immediately at the transcription initiation site of the SP6 promoter (G underlined). Since the Bal31 deletion had removed all restriction sites of the multicloning site of the original plasmid, these were restored by cloning a PvuI-NcoI fragment from the new variant into another variant of pGEM1 (pDH101) that had an NcoI site inserted at its HindIII position in the polylinker. This created the plasmid pDH201. Finally, the adaptor used for cloning the SFV cDNA was inserted into pDH201 between the EcoRI and PvuII sites to create plasmid pPLH211 (Fig. 4B). This plasmid was then used as recipient for SFV cDNA fragments in the assembly of the

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or a few nucleotides, which differ from those shown in Fig. 5, could also be useful as vectors, even if these might be less efficient as illustrated above with the SFV cDNA sequence lacking the first 5'-G nucleotide in Fig. 5.

Example 2.

In this example the construction of SFV DNA expression vectors is disclosed.

The cDNA clone coding for the complete genome of SFV obtained in Example 1 was used to construct a SFV DNA expression vector by deletion of the coding region of the 26S structural genes to make way for heterologous inserts. However, the nonstructural coding region, which is required for the production of the nsP1-4 replicase complex is preserved. RNA replication is dependent on short 5' (nt 1-247) (53, 54, 55) and 3' (nt 11423-11441) sequence elements (56, 57), and therefore, also these had to be included in the vector construct, as had the 26S promoter just upstream of the C gene (17, 18).

As is shown in Fig. 7, first, the XbaI (6640)-NsiI (8927) fragment from the SFV cDNA clone pSP6-SFV4 from Example 1 was cloned into pGEM7Zf(+)(Promega Corp., WI, USA) (Step A). From the resulting plasmid, pGEM7Zf(+)-SFV, the EcoRI fragment (SFV coordinates 7391 and 88746) was cloned into M13mp19 to insert a BamHI - XmaI - SmaI polylinker sequence immediately downstream from the 26S promoter site using site-directed mutagenesis (step B). Once the correct mutants had been verified by sequencing from M13 ssDNA (single stranded), the EcoRI fragments were reinserted into pGEM7Zf(+)-SFV (step C) and then cloned back as XbaI-NsiI fragments into pSP6-SFV4 (step D). To delete the major part of the cDNA region coding for the structural proteins of SFV, these plasmids were then cut with AsuII (7783) and NdeI (11033), blunted using Klenow fragment in the presence of all four nucleotides, and religated to create the

final vectors designated pSFV1, pSFV2 and pSFV3, respectively (step E). The vectors retain the promoter region of the 26S subgenomic RNA and the last 49 amino acids of the E1 protein as well as the complete non-coding 3' end of the SFV genome.

In the vectors the subgenomic (26S) protein coding portion has been replaced with a polylinker sequence allowing the insertional cloning of foreign cDNA sequences under the 26S promoter. As is shown in Fig. 8 these three vectors have the same basic cassette inserted downstream from the 26S promoter, i.e. a polylinker (BamHI-SmaI-XmaI) followed by a translational stop-codons in all three reading frames. The vectors differ as to the position where the polylinker cassette has been inserted. In pSFV1 the cassette is situated 31 bases downstream of the 26S transcription initiation site. The initiation motive of the capsid gene translation is identical to the consensus sequence (58). Therefore, this motive has been provided for in pSFV2, where it is placed immediately after the motive of the capsid gene. Finally, pSFV3 has the cassette placed immediately after the initiation codon (AUG) of the capsid gene. Sequencing primers (SP) needed for checking both ends of an insert have been designed to hybridize either to the 26S promoter region (SP1), or to the region following the stop codon cassette (SP2).

Note that the 26S promoter overlaps with the 3'-end of the nsP4 coding region. For pSFV2, the cloning site is positioned immediately after the translation initiation site of the SFV capsid gene. For pSFV3, the cloning site is positioned three nucleotides further downstream, i.e. immediately following to the initial AUG codon of the SFV capsid gene. The three translation stop codons following the polylinker are boxed. The downstream sequencing primer (SP1) overlaps with the 26S promoter, and the upstream sequencing primer (SP2)

overlaps the XmaIII site.

### Example 3

In this example an in vivo packaging system encompassing helper virus vector constructs is prepared.

5       The system allows SFV variants defective in structural protein functions, or recombinant RNAs derived from the expression vector construct obtained in Example 2, to be packaged into infectious virus particles. Thus, this system allows recombinant RNAs to be introduced into cells by normal infection. The helper vector, called pSFV-Helper1, is constructed by deleting the region between the restriction endo-  
10       nuclease sites AccI (308) and AccI (6399) of pSP6-SFV4 obtained in Example 1 by cutting and religation as shown in Fig. 7, step F. The vector retains the 5' and  
15       3' signals needed for RNA replication. Since almost the complete nsP region of the Helper vector is deleted, RNA produced from this construct will not replicate in the cell due to the lack of a functional replicase  
20       complex. As is shown in Fig. 9, after transcription in vitro of pSFV1-recombinant and helper cDNAs, helper RNA is cotransfected with the pSFV1 - recombinant derivative, the helper construct providing the structural proteins needed to assemble new virus particles, and  
25       the recombinant providing the nonstructural proteins needed for RNA replication, SFV particles comprising recombinant genomes being produced. The cotransfection is preferably produced by electroporation as is disclosed in Example 6 and preferably BHK cells are used  
30       as host cells.

35       To package the RNA a region at the end of nsP1 is required, an area which has been shown to bind capsid protein (57, 59). Since the Helper lacks this region, RNA derived from this vector will not be packaged and hence, transfections with recombinant and Helper produces only virus particles that carry recombinant-derived RNA. It follows that these viruses cannot be

passed further and thus provide a one-step virus stock. The advantage is that infections with these particles will not produce any viral proteins.

#### Example 4

5 This example illustrates the construction of variants of the full-length SFV cDNA clone from Example 1 that allow insertion of foreign DNA sequences encoding foreign epitopes, and the production of recombinant (chimaeric) virus carrying said foreign epitopes as  
10 integral parts of the p62, E2 or E1 spike proteins.

To this end, a thorough knowledge of the function, topology and antigenic structure of the E2 and E1 envelope proteins has been of the essence. Earlier studies on the pathogenicity of alphaviruses have shown  
15 that antibodies against E2 are type-specific and have good neutralizing activity while those against E1 generally are group-specific and are nonneutralizing (5). However, not until recently have antigenic sites of the closely related alphaviruses SFV, Sindbis, and  
20 Ross River been mapped and correlated to the level of amino acid sequence (60, 61, 62, 63). These studies have shown that the most dominant sites in question are at amino acid positions 216, 234 and 246-251 of the SFV E2 spike protein. Interestingly, these three sites are  
25 exactly the same as the ones predicted by computer analysis. In the present example domain 246-251 was used, since this area has a highly conserved structure and hydropathy profile within the group of alpha-viruses. Insertion of a gene encoding a foreign epitope  
30 into the 246-251 region of the pSP6-SFV4 p62 protein yields particles with one new epitope on each heterodimer, i.e. 240 copies.

To create a unique restriction endonuclease site that would allow specific insertion of foreign epitopes into  
35 the E2 portion of the SFV genome, a BamHI site was inserted by site directed mutagenesis using the oligonucleotide 5'-GATCGGCCTAGGAGCCGAGAGCCC.

Example 5

In this example a conditionally lethal variant of SFV is constructed from the SFV cDNA obtained in Example 1, which variant carries a mutation in the p62 protein resulting in a noncleavable form of said protein, with the result that this variant as such cannot infect new host cells, unless first cleaved with exogenously added protease.

As illustrated in Fig. 10, this construct can be advantageously used as a vaccine carrier for foreign epitopes, since this form of the virus cannot enter new host cells although assembled with wild type efficiency in transfected cells. The block can be overcome by trypsin treatment of inactive virus particles. This converts the particle into a fully entry-competent form which can be used for amplification of this virus variant stock.

Once activated the SFV variant will enter cells normally through the endocytic pathway and start infection. Viral proteins will be made and budding takes place at the plasma membrane. However, all virus particles produced will be of inactive form and the infection will thus cease after one round of replication. The reason for the block in infection proficiency is a mutation which has been introduced by site directed mutagenesis into the cleavage site of p62. This arginine to leucine substitution (at amino acid position 66 of the E3 portion of the p62 protein) changes the consensus features of the cleavage site so that it will not be recognized by the host cell proteinase that normally cleaves the p62 protein to the E2 and E3 polypeptides during transport to the cell surface. Instead, only exogenously added trypsin will be able to perform this cleavage, which in this case occurs at the arginine residue 65 immediately preceding the original cleavage site. As this cleavage regulates the activation of the entry function potential of the

virus by controlling the binding of the entry spike subunit, the virus particle carrying only uncleaved p62 will be completely unable to enter new host cells.

5 The creation of the cleavage deficient mutation E2 has been described earlier (29). An Asu1 - Nsa1 fragment spanning this region was then isolated and cloned into the full-length cDNA clone pSP6-SFV4.

#### Example 6

10 In this example transfection of BHK cells with SFV RNA molecules transcribed in vitro from full-length cDNA from Example 1 or variants thereof or the SFV vectors from Example 2, which comprise exogenous DNA, is disclosed. The transfection is carried out by electroporation which is shown to be very efficient at  
15 optimized conditions.

BHK cells were transfected with the above SFV RNA molecules by electroporation and optimal conditions were determined by varying parameters like temperature, voltage, capacitance, and number of pulses. Optimal  
20 transfection was obtained by 2 consecutive pulses of 1.5 kV at 25  $\mu$ F, under which negligible amounts of cells were killed. It was found that it was better to keep the cells at room temperature than at 0°C during the whole procedure. Transfection by electroporation was also measured as a function of input RNA. As  
25 expected, an increase in transfection frequency was not linearly dependent on RNA concentration, and about 2  $\mu$ g of cRNA were needed to obtain 100 % transfection.

On comparison with conventional transfection, this is  
30 a great improvement. For example, with DEAE-Dextran transfection optimally, only 0.2 % of the cells were transfected.

#### Example 7

35 This example illustrates heterologous gene expression driven by the SFV vector, pSFV1 from Example 2, for genes encoding the 21 kD cytoplasmic mouse dihydrofolate reductase (dhfr), the 90 kD membrane protein

human transferrin receptor (TR), and finally the 14 kD secretory protein chicken lysozyme. The dhfr gene was isolated from pGEM2-dhfr (64) as a BamHI-HindIII fragment blunted with Klenow fragment and inserted into SmaI-cut pSFV1. The transferrin receptor gene was first cloned from pGEM1-TR (64, 65) as an XbaI-EcoRI fragment into pGEM7ZF(+) and subsequently from there as a BamHI fragment into pSFV1. Finally, a BamHI fragment from pGEM2 carrying the lysozyme gene (21) was cloned into pSFV1.

To study the expression of the heterologous proteins, in vitro-made RNA of the dhfr and TR constructs was electroporated into BHK cells. RNA of wild type SFV was used as control. At different time points post electroporation (p.e.) cells were pulse-labeled for 10 min followed by a 10 min chase, whereafter the lysates were analyzed by gel electrophoresis and autoradiography. The results are shown in Figure 11. More specifically, BHK cells were transfected with RNAs of wild type SFV, pSFV1-dhfr, and pSFV1-TR, pulse-labeled at 3, 6, 9, 12, 15 and 24 h p.e. Equal amounts of lysate were run on a 12 % gel. The 9 h sample was also used in immunoprecipitation (IP) of the SFV, the dhfr and the transferrin receptor proteins. Cells transfected with pSFV1-lysozyme were pulse-labeled at 9 h p.e. and then chased for the times (hours) indicated. An equal portion of lysate or medium was loaded on the 13,5 % gel. IP represents immunoprecipitation from the 1 h chase lysate sample. The U-lane is lysate of labeled but untransfected cells. At 3 h p.e. hardly any exogenous proteins were made, since the incoming RNA starts with minus strand synthesis which does not peak until about 4-5 h p.e. (5). At this time point, almost all labeled proteins were of host origin. In contrast, at 6 h p.e. the exogenous proteins were synthesized with great efficiency, and severe inhibition of host protein synthesis was evident. This was even more striking at 9 h

p.e., when maximum shut down had been reached. Efficient production of the heterologous proteins continued up to 24 h p.e., after which production slowed down (data not shown), indicating that the cells had entered a stationary phase.

5 Since chicken lysozyme is a secretory protein, its expression was analyzed both from cell lysates and from the growth medium. Cells were pulse-labeled at 9 h p.e. and then chased up to 8 h. The results are shown in Fig. 11. Although lysozyme was slowly secreted, almost all labeled material was secreted to the medium during the chase.

#### Example 8

15 This example illustrates the present in vivo packaging system.

In vitro-made RNA of pSFV1-TR was mixed with Helper RNA at different ratios and these mixtures were co-transfected into BHK cells. Cells were grown for 24 h after which the culture medium was collected and the virus particles pelleted by ultracentrifugation. The number of infectious units (i.u.) was determined by immunofluorescence. It was found that a 1:1 ratio of Helper and recombinant most efficiently produced infectious particles, and on the average  $5 \times 10^6$  cells yielded  $2.5 \times 10^9$  i.u. The infectivity of the virus stock was tested by infecting BHK cells at different multiplicities of infection (m.o.i.). In Fig. 11 the results for expression of human transferrin receptor in BHK cells after infection by such in vivo packaged particles carrying pSFV1-TR recombinant RNA is shown to the lower right. 200  $\mu$ l of virus diluted in MEM (including 0,5% BAS and 2 mM glutamine) was overlaid on cells to give m.o.i. values ranging from 5 to 0.005. After 1 h at 37°C, complete BHK medium was added and growth continued for 9 h, at which time a 10 min pulse (100  $\mu$ Ci  $^{35}$ S-methionine/ml) and 10 min chase was performed, and the cells dissolved in lysis buffer. 10



5  $\mu$ l out of the 300  $\mu$ l lysate (corresponding to 30,000 cells) was run on the 10 % gel, and the dried gel was exposed for 2 h at  $-70^{\circ}\text{C}$ . Due to the high expression level, only 3,000 cells are needed to obtain a distinct band on the autoradiograph with an over night exposure.

Thus, it was found that efficient protein production and concomitant hos protein shut-off occurred at about 1 i.u. per cell. Since one SFV infected cell produces on the average  $10^8$  capsid protein molecules, it follows that a virus stock produced from a single electroporation can be used to produce  $10^{17}$  protein molecules equaling about 50 mg of protein.

10 From the foregoing experimental results it is obvious that the present invention is related to very useful and efficient expression system which lacks several of the disadvantages of the hitherto existing expression system. The major advantages of the present system are shortly summarized as follows:

20 (1) High titre recombinant virus stocks can be produced in one day by one transfection experiment. There is no need for selection/screening, plaque purification and amplification steps. This is appreciated since an easy production of recombinant virus is especially important in experiments where the phenotypes of large series of mutants have to be characterized.

25 (2) The recombinant virus stock is free from helper virus since only the recombinant genome but not the helper genome contains a packaging signal.

30 (3) The recombinant virus can be used to infect the recombinant genome in a "natural" and nonleakey way into a large variety of cells including insect and most higher eucaryotic cell types. Such a wide host range is very useful for an expressions system

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especially when cell-type-specific posttranslational modification reactions are required for the activity of the expressed protein.

- (4) The level of protein expression obtained is extremely high, the level corresponding to those of the viral proteins during infection. There is also a host cell protein shut-off which makes it possible to follow the foreign proteins clearly in cell lysates without the need for antibody mediated antigen concentration. This will facilitate DNA expression experiments in cell biology considerably. Furthermore, problems of interference by the endogenous counter part to an expressed protein (i.e. homo-oligomerization reactions) can be avoided.

#### Example 9

This example illustrates epitope carriers.

A very important example where vaccine development is of the utmost importance concerns the acquired immunodeficiency syndrome (AIDS) caused by the human immunodeficiency virus HIV-1 (66, 67). So far, all attempts to produce an efficient vaccine against HIV-1 have failed, although there was a very recent report that vaccination with disrupted SIV-1 (Simian immunodeficiency virus) to a certain extent may give protection against infections of that virus (68). However, development of safe and effective vaccine against HIV-1 will be very difficult due to the biological properties of the virus. In the present example one epitope of HIV-1 was inserted into an antigenic domain of the E2 protein of SFV. The epitope used is located in glycoprotein gp120 of HIV-1, spanning amino acids 309-325. This forms the variable loop of HIV-1 and is situated immediately after an N-glycosylated site.

A chimera was constructed where the 309-325 epitope of HIV was inserted into the BamHI site using cassette

insertion of ready-made oligonucleotides encoding the HIV epitope. The required base substitutions at the BamHI site did not lead to any amino acid changes in the vector, although two amino acids (Asp and Glu) changed places. This change did not have any deleterious effect since in vitro made vector RNA induced cell infection with wild type efficiency. Fig. 12 shows the sequences in the area of interest in the epitope carrier. In preliminary experiments, it has been shown that chimaeric proteins were produced. The proteins can be immunoprecipitated with anti-HIV antibodies. It is to be expected that these are also used for production of chimaeric virus particles that can be used for vaccine preparation against HIV. Such particles are shown in Fig. 12, lower part.

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Claims

1. An RNA molecule derived from an alphavirus RNA genome and capable of efficient infection of animal host cells, which RNA molecule comprises the complete alphavirus RNA genome regions, which are essential to replication of the said alphavirus RNA, and further comprises an exogenous RNA sequence capable of expressing its function in said host cell, said exogenous RNA sequence being inserted into a region of the RNA molecule which is non-essential to replication thereof.
2. The RNA of claim 1, wherein the said alphavirus is Semliki Forest virus (SFV).
3. The RNA of claim 1 or 2, wherein the exogenous RNA sequence encodes a protein, a polypeptide or a peptide sequence defining an exogenous antigenic epitope or determinant.
4. The RNA of claim 3 wherein the exogenous RNA sequence encodes an epitope sequence of a structural protein of an immunodeficiency virus inclusive of the human immunodeficiency virus (HIV) types.
5. The RNA of any preceding claim, wherein the alphavirus derived RNA molecule regions comprise a 5' terminal portion, the coding region(s) for non structural proteins required for RNA replication, the subgenome promoter region and a 3' terminal portion of said viral RNA.
6. The RNA of claim 2, 3 or 5, wherein the exogenous RNA sequence encodes a foreign polypeptide or protein and is integrated into the SFV subgenomic 26S RNA substituting deleted parts thereof.
7. The RNA of claim 2, 3, 4 or 5, wherein the exogenous RNA sequence encodes a foreign viral epitopic peptide sequence and is located in a region of the RNA coding for structural alphavirus proteins enabling the exogenous RNA to be expressed as said viral epitope as part of the matured virus particle.
8. The RNA of claim 2, 3, 4 or 5, wherein the exogenous RNA sequence encodes a foreign viral epitopic peptide sequence inserted into the p62 spike precursor subunit encoding region of the SFV genome.
9. An RNA expression vector comprising the RNA of any preceding claim packaged into infectious particles comprising the RNA within the alphavirus nucleocapsid and surrounded by membrane with alphavirus spike proteins.

10. The vector of claim 9, wherein the RNA has a total size corresponding to the wild type alphavirus RNA genome or deviating therefrom to an extent compatible with package of the RNA into the infectious particles.

5 11. DNA transcription vector comprising a cDNA having one strand complementary to the RNA of any of claims 1 to 8.

12. A DNA expression vector comprising a full-length or partial cDNA complementary to alphavirus RNA or parts thereof and located immediately downstream of the SP6 RNA polymerase promoter and having a 5'ATGG or 5'GATGG or any other 5' terminus and a TTTCCA<sub>6</sub>ACTAGT or any other 3' terminus.

13. The vector of claim 12 having portions of the viral cDNA deleted, the deletions comprising the complete or part of the region(s) encoding the virus structural proteins, and further comprising an integrated polylinker region, which may correspond to BamHI-SmaI-XmaI, inserted at a location which enables an exogenous DNA fragment encoding a foreign polypeptide or protein to be inserted into the vector cDNA for subsequent expression in an animal host cell.

20 14. The vector of claim 12 or 13 wherein the alphavirus is SFV.

15. The vector of claim 12 or 14 comprising full-length cDNA and further comprising an exogenous DNA fragment encoding a foreign epitopic peptide sequence or antigenic determinant inserted into a region of the viral structural proteins.

25 16. The vector of claim 15 wherein the exogenous DNA fragment is inserted into the p62 spike precursor subunit encoding region of the SFV cDNA.

17. The vector of any preceding claim comprising an SFV derived cDNA which carries a conditionally lethal SFV mutation in the region encoding the p62 cleavage site, a cellularly uncleavable but extracellularly cleavable form of p62 being expressed.

30 18. The vector of claim 13 comprising SFV-derived cDNA, the vector being pSFV1, pSFV2 or pSFV3 having a structure as shown in Fig. 8.

35 19. An RNA transcript derived from transcription of the DNA-vector of any of claims 12-18 carrying an exogenous DNA fragment.

40 20. A method to produce the vector of claim 9 or 10



wherein the alphavirus derived RNA lacks part of or the complete region(s) encoding the structural viral proteins, the method comprising cotransfection of animal host cells with the RNA transcript of claim 19, wherein the alphavirus RNA lacks part(s) of or the complete region(s) encoding the viral structural proteins, with helper RNA transcribed in vitro from a helper DNA vector and culturing the host cells.

21. The method of claim 20 wherein the cotransfection is produced by electroporation of the host cells.

22. Helper vector for use in the method according to claim 20 or 21, said vector being comprised of the DNA vector of claim 12 wherein the regions encoding non structural virus proteins are almost completely deleted, including sequences encoding RNA signals for packaging of RNA into nucleocapsid particles, but the 5' and 3' signals needed for RNA replication and the region encoding the promoter for the structural sub-genome are in addition to those encoding the structural region preserved.

23. Helper vector of claim 22 wherein the cDNA has its origin from SFV and the deletion extends from the AccI (308) to the AccI (6399) restriction endonuclease site of the full-length cDNA vector of claim 12.

24. Helper vector of claim 22 and 23 where the structural region contains the mutation described in claim 17 or another conditionally lethal mutation.

25. The method of claim 20 wherein cells transformed to produce helper RNA according to claims 20, 22 or 23 are transfected with RNA transcript of claim 19.

26. A host cell of animal origin transformed with the RNA of any of claims 1-8, the DNA transcription vector of claims 11 or the DNA vector of any of claims 12-18 carrying an exogenous DNA fragment.

27. The host cell of claim 26 wherein the cell is an avian, a mammalian, a reptilian, an amphibian, an insecticidal or a fish cell.

28. The host cell of claim 27 which is the hamster BHK cell.

29. A method to produce the transformed host cell of claim 26, 27 or 28 comprising transfection of the cell with the RNA of any of claim 1-8, with the cDNA of claim 11 or of any of

claims 12-18 carrying an exogenous DNA fragment or infection of the cell with the infectious viral particles of claim 9 or 10.

30. The method of claim 29 wherein the transfection is produced by electroporation of the host cell.

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31. A method for the production of a polypeptide or protein comprising infection of animal host cells with infectious particles according to claim 9 or 10, containing exogenous RNA encoding said polypeptide or protein and produced according to method of claim 20 or 21, culturing the said transformed cells to express the exogenous RNA and isolation and purification of the product formed by said expression.

10

32. A method for the production of a polypeptide or protein comprising in vitro transcription of the cDNA of the vector of any of claims 11-18 carrying an exogenous DNA fragment coding for the polypeptide or protein, transfection of animal host cells with the produced RNA transcript, transformed animal host cells being obtained harbouring the RNA transcript, culturing the said transformed cells to express the exogenous RNA and isolation and purification of the product formed by said expression.

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33. The method of claim 32 wherein the vector cDNA is comprised of the cDNA of the vector of claim 17 carrying the exogenous DNA fragment.

25

34. An antigen consisting of a chimaeric alphavirus having an exogenous epitopic peptide sequence or antigenic determinant inserted into its structural proteins.

35. The antigen of claim 34 wherein the chimaeric alphavirus is derived from SFV.

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36. The antigen of claim 34 or 35, wherein the exogenous epitopic peptide sequence is comprised of an epitopic peptide sequence derived from a structural protein of a virus belonging to the immunodeficiency virus class inclusive of the human immunodeficiency virus types.

35

37. Vaccine preparation comprising the antigen of claim 34, 35 or 36 as immunizing component.

38. Vaccine of claim 37 wherein the chimaeric alphavirus is attenuated by comprising the conditionally lethal SFV mutation of claim 17, an amber (stop codon) a temperature sensitive mutation or other mutation in its genome.

40

39. A method for the production of an antigen of claim

34, 35 or 36 comprising

a) in vitro transcription of the cDNA of the vector of any of claims 11-18 carrying an exogenous DNA fragment encoding the foreign epitopic peptide sequence or antigenic determinant and transfection of animal host cells with the produced RNA transcript, or

b) transfection of animal host cells with the said cDNA of the above step a),

culturing the transfected cells and recovering the chimaeric alphavirus antigen.

40. The method of claim 32, 33 or 39 wherein the transfection is produced by electroporation of the host cell.

41. A method for the production of an antigen in an organism by using in vivo infection with infectious particles according to claim 9 or 10 containing exogenous RNA encoding an exogenous epitopic peptide sequence or antigenic determinant, and produced according the claim 20 or 21.

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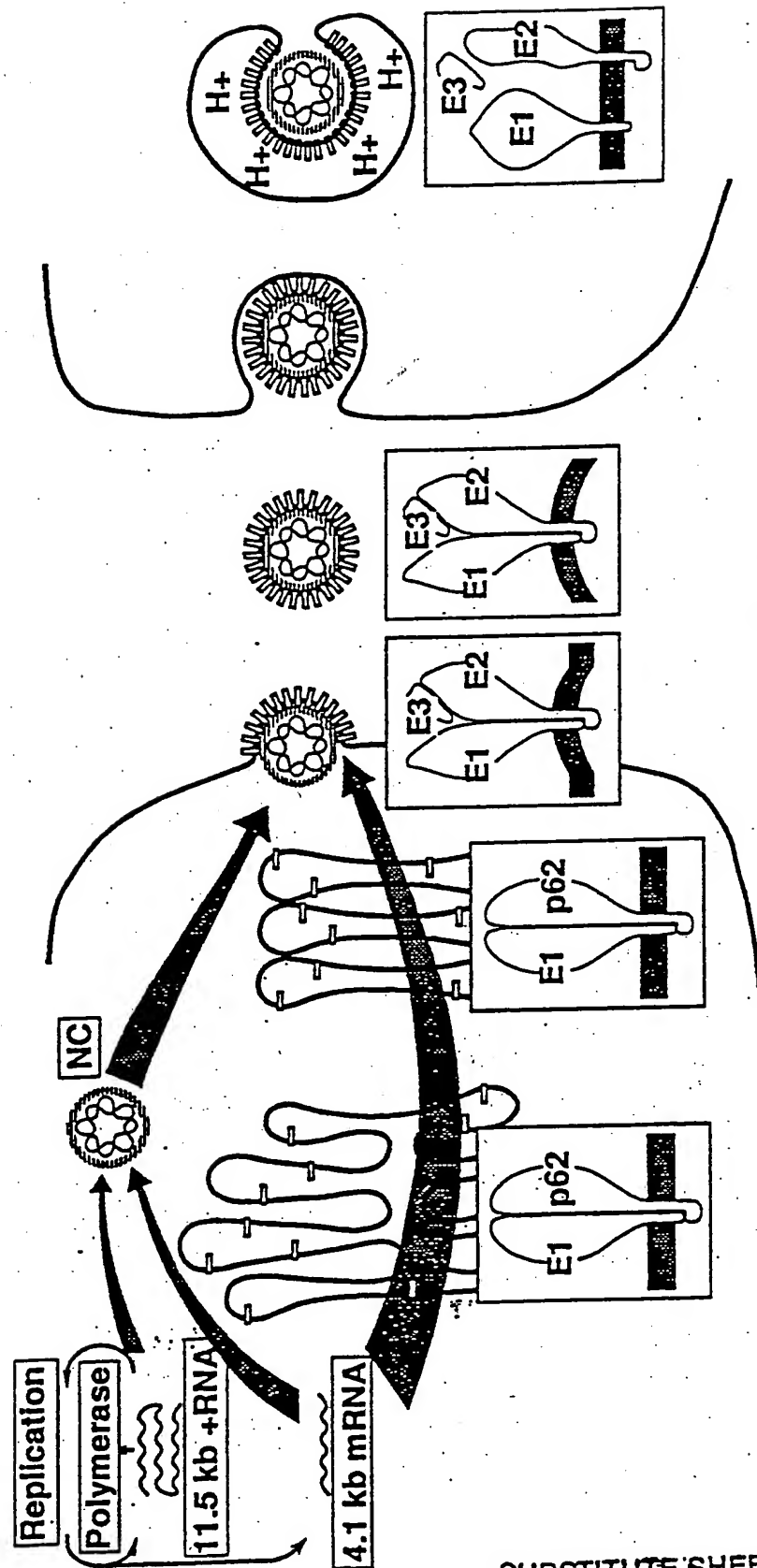


Figure 1

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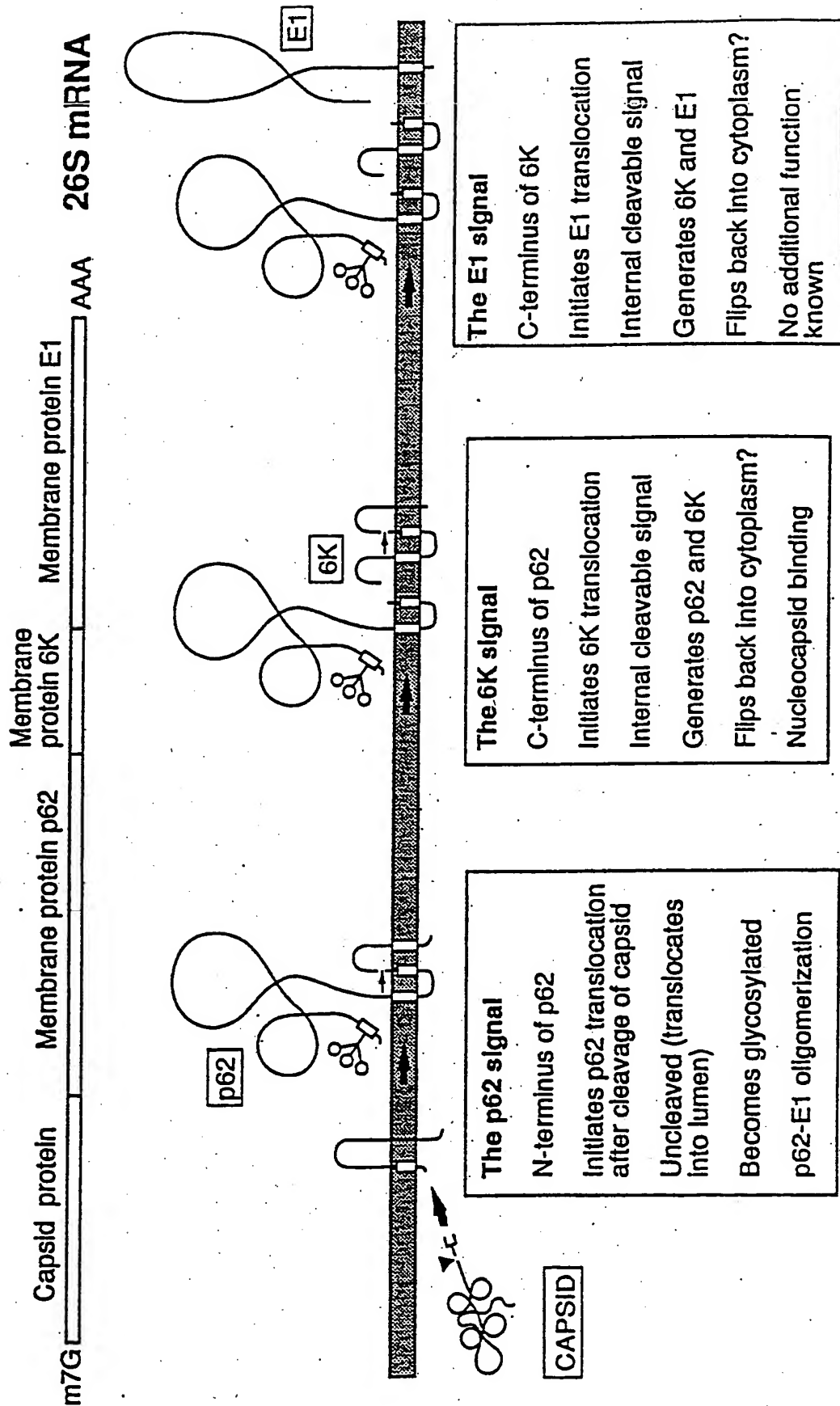


Figure 2

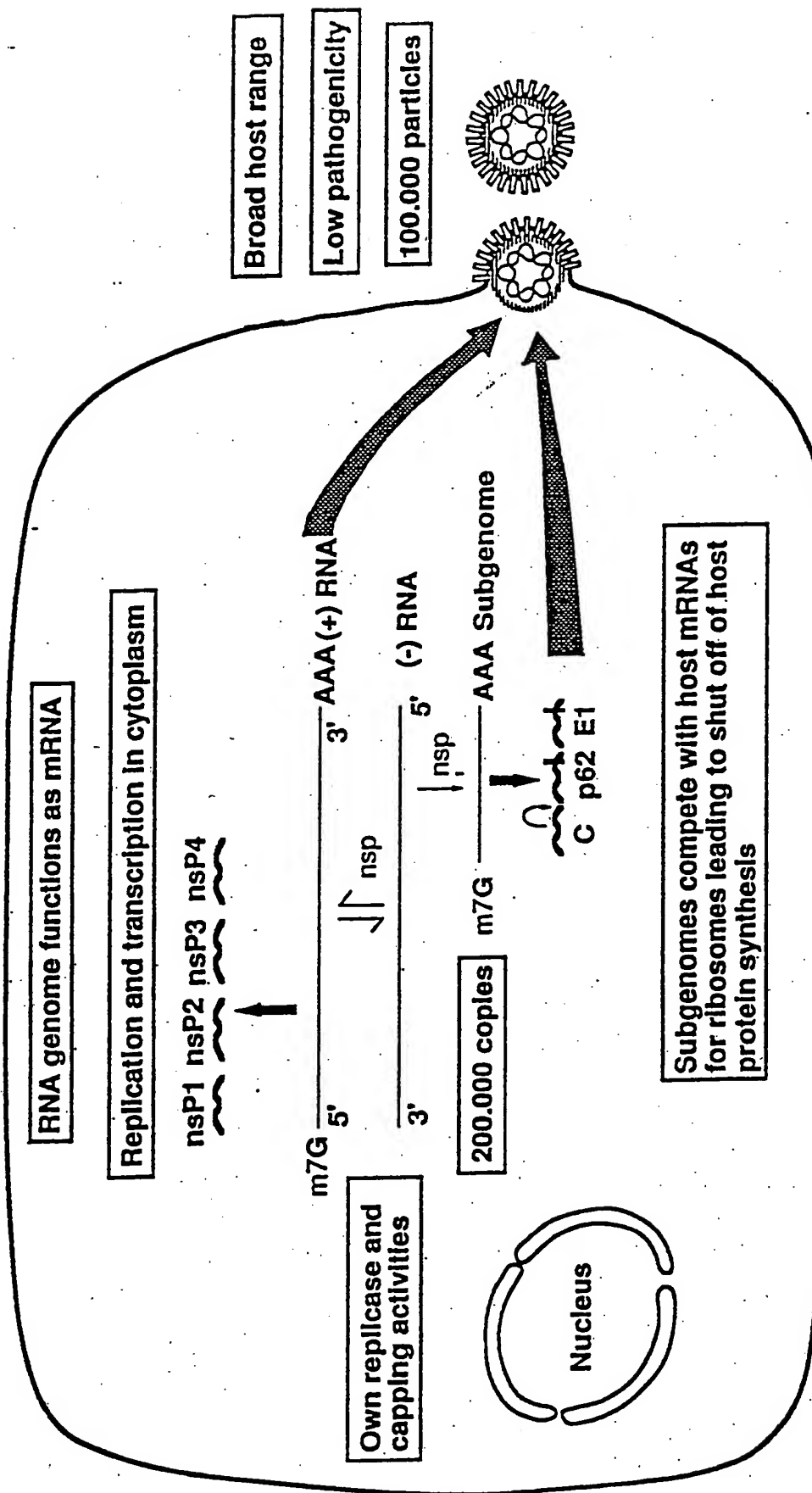


Figure 3

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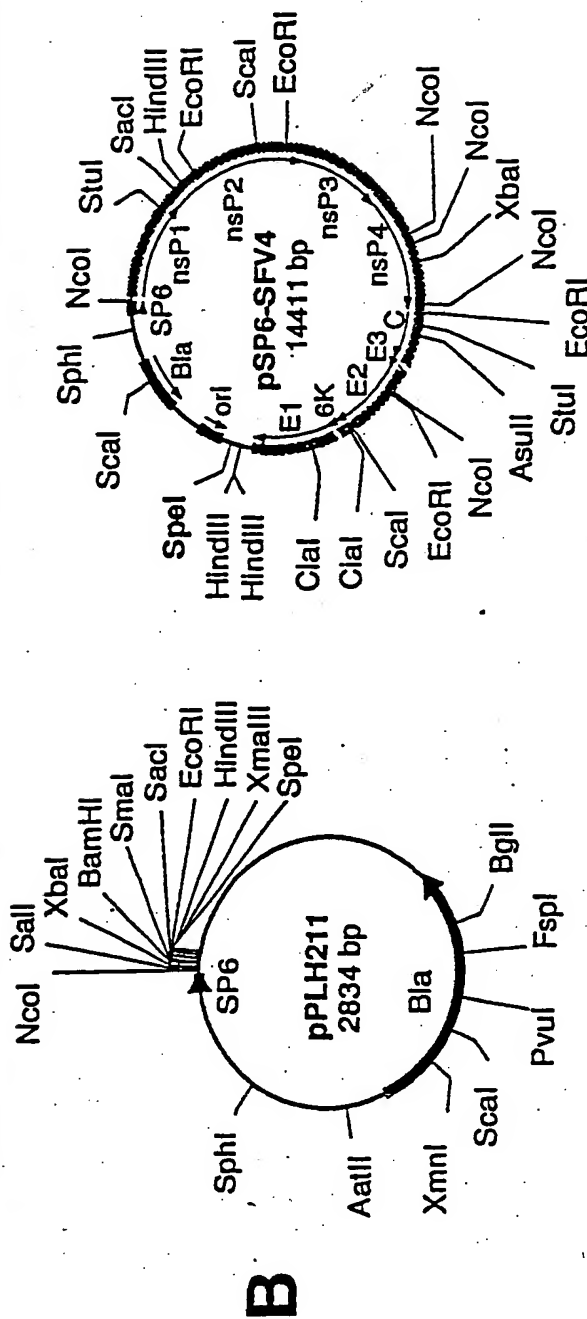
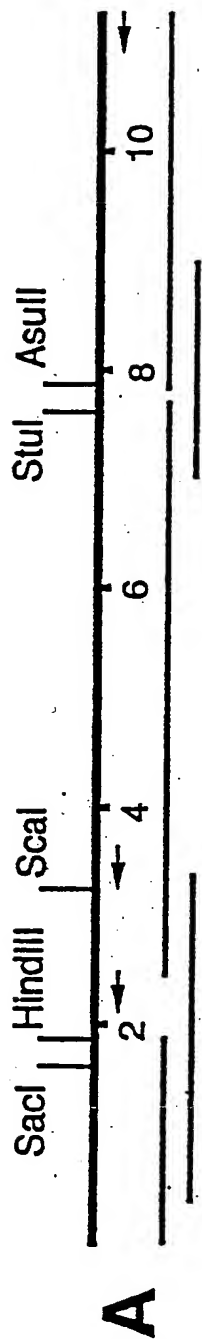


Figure 4



Figure 5 (1)

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GATGGCGGAT GTGTGACATA CACGACGCCA AAAGATTTTG TTCCAGCTCC TGCCACCTCC 60  
 GCTACGCGAG AGATTAACCA CCCACG ATG GCC GCC AAA GTG CAT GTT GAT ATT 113  
 Met Ala Ala Lys Val His Val Asp Ile  
 5

GAG GCT GAC AGC CCA TTC ATC AAG TCT TTG CAG AAG GCA TTT CCG 158  
 Glu Ala Asp Ser Pro Phe Ile Lys Ser Leu Gln Lys Ala Phe Pro  
 10 15 20

TCG TTC GAG GTG GAG TCA TTG CAG GTC ACA CCA AAT GAC CAT GCA 203  
 Ser Phe Glu Val Glu Ser Leu Gln Val Thr Pro Asn Asp His Ala  
 25 30 35

AAT GCC AGA GCA TTT TCG CAC CTG GCT ACC AAA TTG ATC GAG CAG 248  
 Asn Ala Arg Ala Phe Ser His Leu Ala Thr Lys Leu Ile Glu Gln  
 40 45 50

GAG ACT GAC AAA GAC ACA CTC ATC TTG GAT ATC GGC AGT GCG CCT 293  
 Glu Thr Asp Lys Asp Thr Leu Ile Leu Asp Ile Gly Ser Ala Pro  
 55 60 65

TCC AGG AGA ATG ATG TCT ACG CAC AAA TAC CAC TGC GTA TGC CCT 338  
 Ser Arg Arg Met Met Ser Thr His Lys Tyr His Cys Val Cys Pro  
 70 75 80

ATG CGC AGC GCA GAA GAC CCC GAA AGG CTC GAT AGC TAC GCA AAG 383  
 Met Arg Ser Ala Glu Asp Pro Glu Arg Leu Asp Ser Tyr Ala Lys  
 85 90 95

AAA CTG GCA GCG GCC TCC GGG AAG GTG CTG GAT AGA GAG ATC GCA 428  
 Lys Leu Ala Ala Ala Ser Gly Lys Val Leu Asp Arg Glu Ile Ala  
 100 105 110

GGA AAA ATC ACC GAC CTG CAG ACC GTC ATG GCT ACG CCA GAC GCT 473  
 Gly Lys Ile Thr Asp Leu Gln Thr Val Met Ala Thr Pro Asp Ala  
 115 120 125

GAA TCT CCT ACC TTT TGC CTG CAT ACA GAC GTC ACG TGT CGT ACG 518  
 Glu Ser Pro Thr Phe Cys Leu His Thr Asp Val Thr Cys Arg Thr  
 130 135 140

GCA GCC GAA GTG GCC GTA TAC CAG GAC GTG TAT GCT GTA CAT GCA 563  
 Ala Ala Glu Val Ala Val Tyr Gln Asp Val Tyr Ala Val His Ala  
 145 150 155

CCA ACA TCG CTG TAC CAT CAG GCG ATG AAA GGT GTC AGA ACG GCG 608  
 Pro Thr Ser Leu Tyr His Gln Ala Met Lys Gly Val Arg Thr Ala  
 160 165 170

TAT TGG ATT GGG TTT GAC ACC ACC CCG TTT ATG TTT GAC GCG CTA 653  
 Tyr Trp Ile Gly Phe Asp Thr Thr Pro Phe Met Phe Asp Ala Leu  
 175 180 185

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Figure 5 (2)

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GCA GGC GCG TAT CCA ACC TAC GCC ACA AAC TGG GCC GAC GAG CAG	698
Ala Gly Ala Tyr Pro Thr Tyr Ala Thr Asn Trp Ala Asp Glu Gln	
190 195 200	
GTG TTA CAG GCC AGG AAC ATA GGA CTG TGT GCA GCA TCC TTG ACT	743
Val Leu Gln Ala Arg Asn Ile Gly Leu Cys Ala Ala Ser Leu Thr	
205 210 215	
GAG GGA AGA CTC GGC AAA CTG TCC ATT CTC CGC AAG AAG CAA TTG	788
Glu Gly Arg Leu Gly Lys Leu Ser Ile Leu Arg Lys Lys Gln Leu	
220 225 230	
AAA CCT TGC GAC ACA GTC ATG TTC TCG GTA GGA TCT ACA TTG TAC	833
Lys Pro Cys Asp Thr Val Met Phe Ser Val Gly Ser Thr Leu Tyr	
235 240 245	
ACT GAG AGC AGA AAG CTA CTG AGG AGC TGG CAC TTA CCC TCC GTA	878
Thr Glu Ser Arg Lys Leu Leu Arg Ser Trp His Leu Pro Ser Val	
250 255 260	
TTC CAC CTG AAA GGT AAA CAA TCC TTT ACC TGT AGG TGC GAT ACC	923
Phe His Leu Lys Gly Lys Gln Ser Phe Thr Cys Arg Cys Asp Thr	
265 270 275	
ATC GTA TCA TGT GAA GGG TAC GTA GTT AAG AAA ATC ACT ATG TGC	968
Ile Val Ser Cys Glu Gly Tyr Val Val Lys Lys Ile Thr Met Cys	
280 285 290	
CCC GGC CTG TAC GGT AAA ACG GTA GGG TAC GCC GTG ACG TAT CAC	1013
Pro Gly Leu Tyr Gly Lys Thr Val Gly Tyr Ala Val Thr Tyr His	
295 300 305	
GCG GAG GGA TTC CTA GTG TGC AAG ACC ACA GAC ACT GTC AAA GGA	1058
Ala Glu Gly Phe Leu Val Cys Lys Thr Thr Asp Thr Val Lys Gly	
310 315 320	
GAA AGA GTC TCA TTC CCT GTA TGC ACC TAC GTC CCC TCA ACC ATC	1103
Glu Arg Val Ser Phe Pro Val Cys Thr Tyr Val Pro Ser Thr Ile	
325 330 335	
TGT GAT CAA ATG ACT GGC ATA CTA GCG ACC GAC GTC ACA CCG GAG	1148
Cys Asp Gln Met Thr Gly Ile Leu Ala Thr Asp Val Thr Pro Glu	
340 345 350	
GAC GCA CAG AAG TTG TTA GTG GGA TTG AAT CAG AGG ATA GTT GTG	1193
Asp Ala Gln Lys Leu Leu Val Gly Leu Asn Gln Arg Ile Val Val	
355 360 365	
AAC GGA AGA ACA CAG CGA AAC ACT AAC ACG ATG AAG AAC TAT CTG	1238
Asn Gly Arg Thr Gln Arg Asn Thr Asn Thr Met Lys Asn Tyr Leu	
370 375 380	
CTT CCG ATT GTG GCC GTC GCA TTT AGC AAG TGG GCG AGG GAA TAC	1283
Leu Pro Ile Val Ala Val Ala Phe Ser Lys Trp Ala Arg Glu Tyr	
385 390 395	

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Figure 5 (3)

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AAG GCA GAC CTT GAT GAT GAA AAA CCT CTG GGT GTC CGA GAG AGG	1328
Lys Ala Asp Leu Asp Asp Glu Lys Pro Leu Gly Val Arg Glu Arg	
400 405 410	
TCA CTT ACT TGC TGC TGC TTG TGG GCA TTT AAA ACG AGG AAG ATG	1373
Ser Leu Thr Cys Cys Cys Leu Trp Ala Phe Lys Thr Arg Lys Met	
415 420 425	
CAC ACC ATG TAC AAG AAA CCA GAC ACC CAG ACA ATA GTG AAG GTG	1418
His Thr Met Tyr Lys Lys Pro Asp Thr Gln Thr Ile Val Lys Val	
430 435 440	
CCT TCA GAG TTT AAC TCG TTC GTC ATC CCG AGC CTA TGG TCT ACA	1463
Pro Ser Glu Phe Asn Ser Phe Val Ile Pro Ser Leu Trp Ser Thr	
445 450 455	
GGC CTC GCA ATC CCA GTC AGA TCA CGC ATT AAG ATG CTT TTG GCC	1508
Gly Leu Ala Ile Pro Val Arg Ser Arg Ile Lys Met Leu Leu Ala	
460 465 470	
AAG AAG ACC AAG CGA GAG TTA ATA CCT GTT CTC GAC GCG TCG TCA	1553
Lys Lys Thr Lys Arg Glu Leu Ile Pro Val Leu Asp Ala Ser Ser	
475 480 485	
GCC AGG GAT GCT GAA CAA GAG GAG AAG GAG AGG TTG GAG GCC GAG	1598
Ala Arg Asp Ala Glu Gln Glu Glu Lys Glu Arg Leu Glu Ala Glu	
490 495 500	
CTG ACT AGA GAA GCC TTA CCA CCC CTC GTC CCC ATC GCG CCG GCG	1643
Leu Thr Arg Glu Ala Leu Pro Pro Leu Val Pro Ile Ala Pro Ala	
505 510 515	
GAG ACG GGA GTC GTC GAC GTC GAC GTT GAA GAA CTA GAG TAT CAC	1688
Glu Thr Gly Val Val Asp Val Asp Val Glu Glu Leu Glu Tyr His	
520 525 530	
GCA GGT GCA GGG GTC GTG GAA ACA CCT CGC AGC GCG TTG AAA GTC	1733
Ala Gly Ala Gly Val Val Glu Thr Pro Arg Ser Ala Leu Lys Val	
535 540 545	
ACC GCA CAG CCG AAC GAC GTA CTA CTA GGA AAT TAC GTA GTT CTG	1778
Thr Ala Gln Pro Asn Asp Val Leu Leu Gly Asn Tyr Val Val Leu	
550 555 560	
TCC CCG CAG ACC GTG CTC AAG AGC TCC AAG TTG GCC CCC GTG CAC	1823
Ser Pro Gln Thr Val Leu Lys Ser Ser Lys Leu Ala Pro Val His	
565 570 575	
CCT CTA GCA GAG CAG GTG AAA ATA ATA ACA CAT AAC GGG AGG GCC	1868
Pro Leu Ala Glu Gln Val Lys Ile Ile Thr His Asn Gly Arg Ala	
580 585 590	
GGC GGT TAC CAG GTC GAC GGA TAT GAC GGC AGG GTC CTA CTA CCA	1913
Gly Gly Tyr Gln Val Asp Gly Tyr Asp Gly Arg Val Leu Leu Pro	
595 600 605	

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Figure 5 (4)

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TGT	GGA	TCG	GCC	ATT	CCG	GTC	CCT	GAG	TTT	CAA	GCT	TTG	AGC	GAG	1958
Cys	Gly	Ser	Ala	Ile	Pro	Val	Pro	Glu	Phe	Gln	Ala	Leu	Ser	Glu	
610					615					620					
AGC	GCC	ACT	ATG	GTG	TAC	AAC	GAA	AGG	GAG	TTC	GTC	AAC	AGG	AAA	2003
Ser	Ala	Thr	Met	Val	Tyr	Asn	Glu	Arg	Glu	Phe	Val	Asn	Arg	Lys	
625					630					635					
CTA	TAC	CAT	ATT	GCC	GTT	CAC	GGA	CCG	TCG	CTG	AAC	ACC	GAC	GAG	2048
Leu	Tyr	His	Ile	Ala	Val	His	Gly	Pro	Ser	Leu	Asn	Thr	Asp	Glu	
640					645					650					
GAG	AAC	TAC	GAG	AAA	GTC	AGA	GCT	GAA	AGA	ACT	GAC	GCC	GAG	TAC	2093
Glu	Asn	Tyr	Glu	Lys	Val	Arg	Ala	Glu	Arg	Thr	Asp	Ala	Glu	Tyr	
655					660					665					
GTG	TTC	GAC	GTA	GAT	AAA	AAA	TGC	TGC	GTC	AAG	AGA	GAG	GAA	GCG	2138
Val	Phe	Asp	Val	Asp	Lys	Lys	Cys	Cys	Val	Lys	Arg	Glu	Glu	Ala	
670					675					680					
TCG	GGT	TTG	GTG	TTG	GTG	GGA	GAG	CTA	ACC	AAC	CCC	CCG	TTC	CAT	2183
Ser	Gly	Leu	Val	Leu	Val	Gly	Glu	Leu	Thr	Asn	Pro	Pro	Phe	His	
685					690					695					
GAA	TTC	GCC	TAC	GAA	GGG	CTG	AAG	ATC	AGG	CCG	TCG	GCA	CCA	TAT	2228
Glu	Phe	Ala	Tyr	Glu	Gly	Leu	Lys	Ile	Arg	Pro	Ser	Ala	Pro	Tyr	
700					705					710					
AAG	ACT	ACA	GTA	GTA	GGA	GTC	TTT	GGG	GTT	CCG	GGA	TCA	GGC	AAG	2273
Lys	Thr	Thr	Val	Val	Gly	Val	Phe	Gly	Val	Pro	Gly	Ser	Gly	Lys	
715					720					725					
TCT	GCT	ATT	ATT	AAG	AGC	CTC	GTG	ACC	AAA	CAC	GAT	CTG	GTC	ACC	2318
Ser	Ala	Ile	Ile	Lys	Ser	Leu	Val	Thr	Lys	His	Asp	Leu	Val	Thr	
730					735					740					
AGC	GGC	AAG	AAG	GAG	AAC	TGC	CAG	GAA	ATA	GTT	AAC	GAC	GTG	AAG	2363
Ser	Gly	Lys	Lys	Glu	Asn	Cys	Gln	Glu	Ile	Val	Asn	Asp	Val	Lys	
745					750					755					
AAG	CAC	CGC	GGG	AAG	GGG	ACA	AGT	AGG	GAA	AAC	AGT	GAC	TCC	ATC	2408
Lys	His	Arg	Gly	Lys	Gly	Thr	Ser	Arg	Glu	Asn	Ser	Asp	Ser	Ile	
760					765					770					
CTG	CTA	AAC	GGG	TGT	CGT	CGT	GCC	GTG	GAC	ATC	CTA	TAT	GTG	GAC	2453
Leu	Leu	Asn	Gly	Cys	Arg	Arg	Ala	Val	Asp	Ile	Leu	Tyr	Val	Asp	
775					780					785					
GAG	GCT	TTC	GCT	TGC	CAT	TCC	GGT	ACT	CTG	CTG	GCC	CTA	ATT	GCT	2498
Glu	Ala	Phe	Ala	Cys	His	Ser	Gly	Thr	Leu	Leu	Ala	Leu	Ile	Ala	
790					795					800					
CTT	GTT	AAA	CCT	CGG	AGC	AAA	GTG	GTG	TTA	TGC	GGA	GAC	CCC	AAG	2543
Leu	Val	Lys	Pro	Arg	Ser	Lys	Val	Val	Leu	Cys	Gly	Asp	Pro	Lys	
805					810					815					

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Figure 5 (5)

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CAA TGC GGA TTC TTC AAT ATG ATG CAG CTT AAG GTG AAC TTC AAC	2588
Gln Cys Gly Phe Phe Asn Met Met Gln Leu Lys Val Asn Phe Asn	
820 825 830	
CAC AAC ATC TGC ACT GAA GTA TGT CAT AAA AGT ATA TCC AGA CGT	2633
His Asn Ile Cys Thr Glu Val Cys His Lys Ser Ile Ser Arg Arg	
835 840 845	
TGC ACG CGT CCA GTC ACG GCC ATC GTG TCT ACG TTG CAC TAC GGA	2678
Cys Thr Arg Pro Val Thr Ala Ile Val Ser Thr Leu His Tyr Gly	
850 855 860	
GGC AAG ATG CGC ACG ACC AAC CCG TGC AAC AAA CCC ATA ATC ATA	2723
Gly Lys Met Arg Thr Thr Asn Pro Cys Asn Lys Pro Ile Ile Ile	
865 870 875	
GAC ACC ACA GGA CAG ACC AAG CCC AAG CCA GGA GAC ATC GTG TTA	2768
Asp Thr Thr Gly Gln Thr Lys Pro Lys Pro Gly Asp Ile Val Leu	
880 885 890	
ACA TGC TTC CGA GGC TGG GCA AAG CAG CTG CAG TTG GAC TAC CGT	2813
Thr Cys Phe Arg Gly Trp Ala Lys Gln Leu Gln Leu Asp Tyr Arg	
895 900 905	
GGA CAC GAA GTC ATG ACA GCA GCA GCA TCT CAG GGC CTC ACC CGC	2858
Gly His Glu Val Met Thr Ala Ala Ala Ser Gln Gly Leu Thr Arg	
910 915 920	
AAA GGG GTA TAC GCC GTA AGG CAG AAG GTG AAT GAA AAT CCC TTG	2903
Lys Gly Val Tyr Ala Val Arg Gln Lys Val Asn Glu Asn Pro Leu	
925 930 935	
TAT GCC CCT GCG TCG GAG CAC GTG AAT GTA CTG CTG ACG CGC ACT	2948
Tyr Ala Pro Ala Ser Glu His Val Asn Val Leu Leu Thr Arg Thr	
940 945 950	
GAG GAT AGG CTG GTG TGG AAA ACG CTG GCC GGC GAT CCC TGG ATT	2993
Glu Asp Arg Leu Val Trp Lys Thr Leu Ala Gly Asp Pro Trp Ile	
955 960 965	
AAG GTC CTA TCA AAC ATT CCA CAG GGT AAC TTT ACG GCC ACA TTG	3038
Lys Val Leu Ser Asn Ile Pro Gln Gly Asn Phe Thr Ala Thr Leu	
970 975 980	
GAA GAA TGG CAA GAA GAA CAC GAC AAA ATA ATG AAG GTG ATT GAA	3083
Glu Glu Trp Gln Glu His Asp Lys Ile Met Lys Val Ile Glu	
985 990 995	
GGA CCG GCT GCG CCT GTG GAC GCG TTC CAG AAC AAA GCG AAC GTG	3128
Gly Pro Ala Ala Pro Val Asp Ala Phe Gln Asn Lys Ala Asn Val	
1000 1005 1010	
TGT TGG GCG AAA AGC CTG GTG CCT GTC CTG GAC ACT GCG GGA ATC	3173
Cys Trp Ala Lys Ser Leu Val Pro Val Leu Asp Thr Ala Gly Ile	
1015 1020 1025	

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Figure 5 (6)

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AGA TTG ACA GCA GAG GAG TGG AGC ACC ATA ATT ACA GCA TTT AAG	3218
Arg Leu Thr Ala Glu Glu Trp Ser Thr Ile Ile Thr Ala Phe Lys	
1030 1035 1040	
GAG GAC AGA GCT TAC TCT CCA GTG GTG CCC TTG AAT GAA ATT TGC	3263
Glu Asp Arg Ala Tyr Ser Pro Val Val Ala Leu Asn Glu Ile Cys	
1045 1050 1055	
ACC AAG TAC TAT GGA GTT GAC CTG GAC AGT GGC CTG TTT TCT GCC	3308
Thr Lys Tyr Tyr Gly Val Asp Leu Asp Ser Gly Leu Phe Ser Ala	
1060 1065 1070	
CCG AAG GTG TCC CTG TAT TAC GAG AAC AAC CAC TGG GAT AAC AGA	3353
Pro Lys Val Ser Leu Tyr Tyr Glu Asn Asn His Trp Asp Asn Arg	
1075 1080 1085	
CCT GGT GGA AGG ATG TAT GGA TTC AAT GCC GCA ACA GCT GCC AGG	3398
Pro Gly Gly Arg Met Tyr Gly Phe Asn Ala Ala Thr Ala Ala Arg	
1090 1095 1100	
CTG GAA GCT AGA CAT ACC TTC CTG AAG GGG CAG TGG CAT ACG GGC	3443
Leu Glu Ala Arg His Thr Phe Leu Lys Gly Gln Trp His Thr Gly	
1105 1110 1115	
AAG CAG GCA GTT ATC GCA GAA AGA AAA ATC CAA CCG CTT TCT GTG	3488
Lys Gln Ala Val Ile Ala Glu Arg Lys Ile Gln Pro Leu Ser Val	
1120 1125 1130	
CTG GAC AAT GTA ATT CCT ATC AAC CGC AGG CTG CCG CAC GCC CTG	3533
Leu Asp Asn Val Ile Pro Ile Asn Arg Arg Leu Pro His Ala Leu	
1135 1140 1145	
GTG GCT GAG TAC AAG ACG GTT AAA GGC AGT AGG GTT GAG TGG CTG	3578
Val Ala Glu Tyr Lys Thr Val Lys Gly Ser Arg Val Glu Trp Leu	
1150 1155 1160	
GTC AAT AAA GTA AGA GGG TAC CAC GTC CTG CTG GTG AGT GAG TAC	3623
Val Asn Lys Val Arg Gly Tyr His Val Leu Leu Val Ser Glu Tyr	
1165 1170 1175	
AAC CTG GCT TTG CCT CGA CGC AGG GTC ACT TGG TTG TCA CCG CTG	3668
Asn Leu Ala Leu Pro Arg Arg Arg Val Thr Trp Leu Ser Pro Leu	
1180 1185 1190	
AAT GTC ACA GGC GCC GAT AGG TGC TAC GAC CTA AGT TTA GGA CTG	3713
Asn Val Thr Gly Ala Asp Arg Cys Tyr Asp Leu Ser Leu Gly Leu	
1195 1200 1205	
CCG GCT GAC GCC GGC AGG TTC GAC TTG GTC TTT GTG AAC ATT CAC	3758
Pro Ala Asp Ala Gly Arg Phe Asp Leu Val Phe Val Asn Ile His	
1210 1215 1220	
ACG GAA TTC AGA ATC CAC CAC TAC CAG CAG TGT GTC GAC CAC GCC	3803
Thr Glu Phe Arg Ile His His Tyr Gln Gln Cys Val Asp His Ala	
1225 1230 1235	

Figure 5 (7)

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ATG AAG CTG CAG ATG CTT GGG GGA GAT GCG CTA CGA CTG CTA AAA	3848
Met Lys Leu Gln Met Leu Gly Gly Asp Ala Leu Arg Leu Leu Lys	
1240 1245 1250	
CCC GGC GGC ATC TTG ATG AGA GCT TAC GGA TAC GCC GAT AAA ATC	3893
Pro Gly Gly Ile Leu Met Arg Ala Tyr Gly Tyr Ala Asp Lys Ile	
1255 1260 1265	
AGC GAA GCC GTT GTT TCC TCC TTA AGC AGA AAG TTC TCG TCT GCA	3938
Ser Glu Ala Val Val Ser Ser Leu Ser Arg Lys Phe Ser Ser Ala	
1270 1275 1280	
AGA GTG TTG CGC CCG GAT TGT GTC ACC AGC AAT ACA GAA GTG TTC	3983
Arg Val Leu Arg Pro Asp Cys Val Thr Ser Asn Thr Glu Val Phe	
1285 1290 1295	
TTG CTG TTC TCC AAC TTT GAC AAC GGA AAG AGA CCC TCT ACG CTA	4028
Leu Leu Phe Ser Asn Phe Asp Asn Gly Lys Arg Pro Ser Thr Leu	
1300 1305 1310	
CAC CAG ATG AAT ACC AAG CTG AGT GCC GTG TAT GCC GGA GAA GCC	4073
His Gln Met Asn Thr Lys Leu Ser Ala Val Tyr Ala Gly Glu Ala	
1315 1320 1325	
ATG CAC ACG GCC GGG TGT GCA CCA TCC TAC AGA GTT AAG AGA GCA	4118
Met His Thr Ala Gly Cys Ala Pro Ser Tyr Arg Val Lys Arg Ala	
1330 1335 1340	
GAC ATA GCC ACG TGC ACA GAA GCG GCT GTG GTT AAC GCA GCT AAC	4163
Asp Ile Ala Thr Cys Thr Glu Ala Ala Val Val Asn Ala Ala Asn	
1345 1350 1355	
GCC CGT GGA ACT GTA GGG GAT GGC GTA TGC AGG GCC GTG GCG AAG	4208
Ala Arg Gly Thr Val Gly Asp Gly Val Cys Arg Ala Val Ala Lys	
1360 1365 1370	
AAA TGG CCG TCA GCC TTT AAG GGA GCA GCA ACA CCA GTG GGC ACA	4253
Lys Trp Pro Ser Ala Phe Lys Gly Ala Ala Thr Pro Val Gly Thr	
1375 1380 1385	
ATT AAA ACA GTC ATG TGC GGC TCG TAC CCC GTC ATC CAC GCT GTA	4298
Ile Lys Thr Val Met Cys Gly Ser Tyr Pro Val Ile His Ala Val	
1390 1395 1400	
GCG CCT AAT TTC TCT GCC ACG ACT GAA GCG GAA GGG GAC CGC GAA	4343
Ala Pro Asn Phe Ser Ala Thr Thr Glu Ala Glu Gly Asp Arg Glu	
1405 1410 1415	
TTG GCC GCT GTC TAC CGG GCA GTG GCC GCC GAA GTA AAC AGA CTG	4388
Leu Ala Ala Val Tyr Arg Ala Val Ala Ala Glu Val Asn Arg Leu	
1420 1425 1430	
TCA CTG AGC AGC GTA GCC ATC CCG CTG CTG TCC ACA GGA GTG TTC	4433
Ser Leu Ser Ser Val Ala Ile Pro Leu Leu Ser Thr Gly Val Phe	
1435 1440 1445	

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CTG TTC GAC CCG ACG GTA CCT TCA GTG GTT AGT CCG CGG AAG TAT 5063  
Leu Phe Asp Pro Thr Val Pro Ser Val Val Ser Pro Arg Lys Tyr  
1645 1650 1655



Figure 5 (9)

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GCC GCA TCT ACG ACG GAC CAC TCA GAT CGG TCG TTA CGA GGG TTT	5108
Ala Ala Ser Thr Thr Asp His Ser Asp Arg Ser Leu Arg Gly Phe	
1660 1665 1670	
GAC TTG GAC TGG ACC ACC GAC TCG TCT TCC ACT GCC AGC GAT ACC	5153
Asp Leu Asp Trp Thr Thr Asp Ser Ser Ser Thr Ala Ser Asp Thr	
1675 1680 1685	
ATG TCG CTA CCC AGT TTG CAG TCG TGT GAC ATC GAC TCG ATC TAC	5198
Met Ser Leu Pro Ser Leu Gln Ser Cys Asp Ile Asp Ser Ile Tyr	
1690 1695 1700	
GAG CCA ATG GCT CCC ATA GTA GTG ACG GCT GAC GTA CAC CCT GAA	5243
Glu Pro Met Ala Pro Ile Val Val Thr Ala Asp Val His Pro Glu	
1705 1710 1715	
CCC GCA GGC ATC GCG GAC CTG GCG GCA GAT GTG CAC CCT GAA CCC	5288
Pro Ala Gly Ile Ala Asp Leu Ala Ala Asp Val His Pro Glu Pro	
1720 1725 1730	
GCA GAC CAT GTG GAC CTC GAG AAC CCG ATT CCT CCA CCG CGC CCG	5333
Ala Asp His Val Asp Leu Glu Asn Pro Ile Pro Pro Pro Arg Pro	
1735 1740 1745	
AAG AGA GCT GCA TAC CTT GCC TCC CGC GCG GCG GAG CGA CCG GTG	5378
Lys Arg Ala Ala Tyr Leu Ala Ser Arg Ala Ala Glu Arg Pro Val	
1750 1755 1760	
CCG GCG CCG AGA AAG CCG ACG CCT GCC CCA AGG ACT GCG TTT AGG	5423
Pro Ala Pro Arg Lys Pro Thr Pro Ala Pro Arg Thr Ala Phe Arg	
1765 1770 1775	
AAC AAG CTG CCT TTG ACG TTC GGC GAC TTT GAC GAG CAC GAG GTC	5468
Asn Lys Leu Pro Leu Thr Phe Gly Asp Phe Asp Glu His Glu Val	
1780 1785 1790	
GAT GCG TTG GCC TCC GGG ATT ACT TTC GGA GAC TTC GAC GAC GTC	5513
Asp Ala Leu Ala Ser Gly Ile Thr Phe Gly Asp Phe Asp Asp Val	
1795 1800 1805	
CTG CGA CTA GGC CGC GCG GGT GCA TAT ATT TTC TCC TCG GAC ACT	5558
Leu Arg Leu Gly Arg Ala Gly Ala Tyr Ile Phe Ser Ser Asp Thr	
1810 1815 1820	
GGC AGC GGA CAT TTA CAA CAA AAA TCC GTT AGG CAG CAC AAT CTC	5603
Gly Ser Gly His Leu Gln Gln Lys Ser Val Arg Gln His Asn Leu	
1825 1830 1835	
CAG TGC GCA CAA CTG GAT GCG GTC CAG GAG GAG AAA ATG TAC CCG	5648
Gln Cys Ala Gln Leu Asp Ala Val Gln Glu Glu Lys Met Tyr Pro	
1840 1845 1850	
CCA AAA TTG GAT ACT GAG AGG GAG AAG CTG TTG CTG CTG AAA ATG	5693
Pro Lys Leu Asp Thr Glu Arg Glu Lys Leu Leu Leu Leu Lys Met	
1855 1860 1865	

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Figure 5 (10)

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CAG ATG CAC CCA TCG GAG GCT AAT AAG AGT CGA TAC CAG TCT CGC	5738
Gln Met His Pro Ser Glu Ala Asn Lys Ser Arg Tyr Gln Ser Arg	
1870 1875 1880	
AAA GTG GAG AAC ATG AAA GCC ACG GTG GTG GAC AGG CTC ACA TCG	5783
Lys Val Glu Asn Met Lys Ala Thr Val Val Asp Arg Leu Thr Ser	
1885 1890 1895	
GGG GCC AGA TTG TAC ACG GGA GCG GAC GTA GGC CGC ATA CCA ACA	5828
Gly Ala Arg Leu Tyr Thr Gly Ala Asp Val Gly Arg Ile Pro Thr	
1900 1905 1910	
TAC GCG GTT CCG TAC CCC CGC CCC GTG TAC TCC CCT ACC GTG ATC	5873
Tyr Ala Val Arg Tyr Pro Arg Pro Val Tyr Ser Pro Thr Val Ile	
1915 1920 1925	
GAA AGA TTC TCA AGC CCC GAT GTA GCA ATC GCA GCG TGC AAC GAA	5918
Glu Arg Phe Ser Ser Pro Asp Val Ala Ile Ala Ala Cys Asn Glu	
1930 1935 1940	
TAC CTA TCC AGA AAT TAC CCA ACA GTG GCG TCG TAC CAG ATA ACA	5963
Tyr Leu Ser Arg Asn Tyr Pro Thr Val Ala Ser Tyr Gln Ile Thr	
1945 1950 1955	
GAT GAA TAC GAC GCA TAC TTG GAC ATG GTT GAC GGG TCG GAT AGT	6008
Asp Glu Tyr Asp Ala Tyr Leu Asp Met Val Asp Gly Ser Asp Ser	
1960 1965 1970	
TGC TTG GAC AGA GCG ACA TTC TGC CCG GCG AAG CTC CGG TGC TAC	6053
Cys Leu Asp Arg Ala Thr Phe Cys Pro Ala Lys Leu Arg Cys Tyr	
1975 1980 1985	
CCG AAA CAT CAT GCG TAC CAC CAG CCG ACT GTA CGC AGT GCC GTC	6098
Pro Lys His His Ala Tyr His Gln Pro Thr Val Arg Ser Ala Val	
1990 1995 2000	
CCG TCA CCC TTT CAG AAC ACA CTA CAG AAC GTG CTA GCG GCC GCC	6143
Pro Ser Pro Phe Gln Asn Thr Leu Gln Asn Val Leu Ala Ala Ala	
2005 2010 2015	
ACC AAG AGA AAC TGC AAC GTC ACG CAA ATG CGA GAA CTA CCC ACC	6188
Thr Lys Arg Asn Cys Asn Val Thr Gln Met Arg Glu Leu Pro Thr	
2020 2025 2030	
ATG GAC TCG GCA GTG TTC AAC GTG GAG TGC TTC AAG CGC TAT GCC	6233
Met Asp Ser Ala Val Phe Asn Val Glu Cys Phe Lys Arg Tyr Ala	
2035 2040 2045	
TGC TCC GGA GAA TAT TGG GAA GAA TAT GCT AAA CAA CCT ATC CGG	6278
Cys Ser Gly Glu Tyr Trp Glu Glu Tyr Ala Lys Gln Pro Ile Arg	
2050 2055 2060	
ATA ACC ACT GAG AAC ATC ACT ACC TAT GTG ACC AAA TTG AAA GGC	6323
Ile Thr Thr Glu Asn Ile Thr Thr Tyr Val Thr Lys Leu Lys, Gly	
2065 2070 2075	

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Figure 5 (11)

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CCG AAA GCT GCT GCC TTG TTC GCT AAG ACC CAC AAC TTG GTT CCG	6368
Pro Lys Ala Ala Ala Leu Phe Ala Lys Thr His Asn Leu Val Pro	
2080	2085 2090
CTG CAG GAG GTT CCC ATG GAC AGA TTC ACG GTC GAC ATG AAA CGA	6413
Leu Gln Glu Val Pro Met Asp Arg Phe Thr Val Asp Met Lys Arg	
2095	2100 2105
GAT GTC AAA GTC ACT CCA GGG ACG AAA CAC ACA GAG GAA AGA CCC	6458
Asp Val Lys Val Thr Pro Gly Thr Lys His Thr Glu Glu Arg Pro	
2110	2115 2120
AAA GTC CAG GTA ATT CAA GCA GCG GAG CCA TTG GCG ACC GCT TAC	6503
Lys Val Gln Val Ile Gln Ala Ala Glu Pro Leu Ala Thr Ala Tyr	
2125	2130 2135
CTG TGC GGC ATC CAC AGG GAA TTA GTA AGG AGA CTA AAT GCT GTG	6548
Leu Cys Gly Ile His Arg Glu Leu Val Arg Arg Leu Asn Ala Val	
2140	2145 2150
TTA CGC CCT AAC GTG CAC ACA TTG TTT GAT ATG TCG GCC GAA GAC	6593
Leu Arg Pro Asn Val His Thr Leu Phe Asp Met Ser Ala Glu Asp	
2155	2160 2165
TTT GAC GCG ATC ATC GCC TCT CAC TTC CAC CCA GGA GAC CCG GTT	6638
Phe Asp Ala Ile Ile Ala Ser His Phe His Pro Gly Asp Pro Val	
2170	2175 2180
CTA GAG ACG GAC ATT GCA TCA TTC GAC AAA AGC CAG GAC GAC TCC	6683
Leu Glu Thr Asp Ile Ala Ser Phe Asp Lys Ser Gln Asp Asp Ser	
2185	2190 2195
TTG GCT CTT ACA GGT TTA ATG ATC CTC GAA GAT CTA GGG GTG GAT	6728
Leu Ala Leu Thr Gly Leu Met Ile Leu Glu Asp Leu Gly Val Asp	
2200	2205 2210
CAG TAC CTG CTG GAC TTG ATC GAG GCA GCC TTT GGG GAA ATA TCC	6773
Gln Tyr Leu Leu Asp Leu Ile Glu Ala Ala Phe Gly Glu Ile Ser	
2215	2220 2225
AGC TGT CAC CTA CCA ACT GGC ACG CGC TTC AAG TTC GGA GCT ATG	6818
Ser Cys His Leu Pro Thr Gly Thr Arg Phe Lys Phe Gly Ala Met	
2230	2235 2240
ATG AAA TCG GGC ATG TTT CTG ACT TTG TTT ATT AAC ACT GTT TTG	6863
Met Lys Ser Gly Met Phe Leu Thr Leu Phe Ile Asn Thr Val Leu	
2245	2250 2255
AAC ATC ACC ATA GCA AGC AGG GTA CTG GAG CAG AGA CTC ACT GAC	6908
Asn Ile Thr Ile Ala Ser Arg Val Leu Glu Gln Arg Leu Thr Asp	
2260	2265 2270
TCC GCC TGT GCG GCC TTC ATC GGC GAC GAC AAC ATC GTT CAC GGA	6953
Ser Ala Cys Ala Ala Phe Ile Gly Asp Asp Asn Ile Val His Gly	
2275	2280 2285

Figure 5 (12)

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GTG ATC TCC GAC AAG CTG ATG GCG GAG AGG TGC GCG TCG TGG GTC 6998  
 Val Ile Ser Asp Lys Leu Met Ala Glu Arg Cys Ala Ser Trp Val  
 2290 2295 2300

AAC ATG GAG GTG AAG ATC ATT GAC GCT GTC ATG GGC GAA AAA CCC 7043  
 Asn Met Glu Val Lys Ile Ile Asp Ala Val Met Gly Glu Lys Pro  
 2305 2310 2315

CCA TAT TTT TGT GGG GGA TTC ATA GTT TTT GAC AGC GTC ACA CAG 7088  
 Pro Tyr Phe Cys Gly Gly Phe Ile Val Phe Asp Ser Val Thr Gln  
 2320 2325 2330

ACC GCC TGC CGT GTT TCA GAC CCA CTT AAG CGC CTG TTC AAG TTG 7133  
 Thr Ala Cys Arg Val Ser Asp Pro Leu Lys Arg Leu Phe Lys Leu  
 2335 2340 2345

GGT AAG CCG CTA ACA GCT GAA GAC AAG CAG GAC GAA GAC AGG CGA 7178  
 Gly Lys Pro Leu Thr Ala Glu Asp Lys Gln Asp Glu Asp Arg Arg  
 2350 2355 2360

CGA GCA CTG AGT GAC GAG GTT AGC AAG TGG TTC CGG ACA GGC TTG 7223  
 Arg Ala Leu Ser Asp Glu Val Ser Lys Trp Phe Arg Thr Gly Leu  
 2365 2370 2375

GGG GCC GAA CTG GAG GTG GCA CTA ACA TCT AGG TAT GAG GTA GAG 7268  
 Gly Ala Glu Leu Glu Val Ala Leu Thr Ser Arg Tyr Glu Val Glu  
 2380 2385 2390

GGC TGC AAA AGT ATC CTC ATA GCC ATG ACC ACC TTG GCG AGG GAC 7313  
 Gly Cys Lys Ser Ile Leu Ile Ala Met Thr Thr Leu Ala Arg Asp  
 2395 2400 2405

ATT AAG GCG TTT AAG AAA TTG AGA GGA CCT GTT ATA CAC CTC TAC 7358  
 Ile Lys Ala Phe Lys Lys Leu Arg Gly Pro Val Ile His Leu Tyr  
 2410 2415 2420

GGC GGT CCT AGA TTG GTG CGT TAA TACACAGAAT TCTGATTATA GCGCACTATT 7412  
 Gly Gly Pro Arg Leu Val Arg  
 2425 2430

ATAGCACC ATG AAT TAC ATC CCT ACG CAA ACG TTT TAC GGC CGC CGG 7459  
 Met Asn Tyr Ile Pro Thr Gln Thr Phe Tyr Gly Arg Arg  
 5 10

TGG CGC CCG CGC CCG GCG GCC CGT CCT TGG CCG TTG CAG GCC ACT 7504  
 Trp Arg Pro Arg Pro Ala Ala Arg Pro Trp Pro Leu Gln Ala Thr  
 15 20 25

CCG GTG GCT CCC GTC GTC CCC GAC TTC CAG GCC CAG CAG ATG CAG 7549  
 Pro Val Ala Pro Val Val Pro Asp Phe Gln Ala Gln Gln Met Gln  
 30 35 40

CAA CTC ATC AGC GCC GTA AAT GCG CTG ACA ATG AGA CAG AAC GCA 7594  
 Gln Leu Ile Ser Ala Val Asn Ala Leu Thr Met Arg Gln Asn Ala  
 45 50 55

Figure 5 (13)

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ATT GCT CCT GCT AGG CCT CCC AAA CCA AAG AAG AAG AAG ACA ACC	7639
Ile Ala Pro Ala Arg Pro Pro Lys Pro Lys Lys Lys Lys Thr Thr	
60 65 70	
AAA CCA AAG CCG AAA ACG CAG CCC AAG AAG ATC AAC GGA AAA ACG	7684
Lys Pro Lys Pro Lys Thr Gln Pro Lys Lys Ile Asn Gly Lys Thr	
75 80 85	
CAG CAG CAA AAG AAG AAA GAC AAG CAA GCC GAC AAG AAG AAG AAG	7729
Gln Gln Gln Lys Lys Lys Asp Lys Gln Ala Asp Lys Lys Lys Lys	
90 95 100	
AAA CCC GGA AAA AGA GAA AGA ATG TGC ATG AAG ATT GAA AAT GAC	7774
Lys Pro Gly Lys Arg Glu Arg Met Cys Met Lys Ile Glu Asn Asp	
105 110 115	
TGT ATC TTC GAA GTC AAA CAC GAA GGA AAG GTC ACT GGG TAC GCC	7819
Cys Ile Phe Glu Val Lys His Glu Gly Lys Val Thr Gly Tyr Ala	
120 125 130	
TGC CTG GTG GGC GAC AAA GTC ATG AAA CCT GCC CAC GTC AAA GGA	7864
Cys Leu Val Gly Asp Lys Val Met Lys Pro Ala His Val Lys Gly	
135 140 145	
GTC ATC GAC AAC GCG GAC CTG GCA AAG CTA GCT TTC AAG AAA TCG	7909
Val Ile Asp Asn Ala Asp Leu Ala Lys Leu Ala Phe Lys Lys Ser	
150 155 160	
AGC AAG TAT GAC CTT GAG TGT GCC CAG ATA CCA GTT CAC ATG AGG	7954
Ser Lys Tyr Asp Leu Glu Cys Ala Gln Ile Pro Val His Met Arg	
165 170 175	
TCG GAT GCC TCA AAG TAC ACG CAT GAG AAG CCC GAG GGA CAC TAT	7999
Ser Asp Ala Ser Lys Tyr Thr His Glu Lys Pro Glu Gly His Tyr	
180 185 190	
AAC TGG CAC CAC GGG GCT GTT CAG TAC AGC GGA GGT AGG TTC ACT	8044
Asn Trp His His Gly Ala Val Gln Tyr Ser Gly Gly Arg Phe Thr	
195 200 205	
ATA CCG ACA GGA GCG GGC AAA CCG GGA GAC AGT GGC CGG CCC ATC	8089
Ile Pro Thr Gly Ala Gly Lys Pro Gly Asp Ser Gly Arg Pro Ile	
210 215 220	
TTT GAC AAC AAG GGG AGG GTA GTC GCT ATC GTC CTG GGC GGG GCC	8134
Phe Asp Asn Lys Gly Arg Val Val Ala Ile Val Leu Gly Gly Ala	
225 230 235	
AAC GAG GGC TCA CGC ACA GCA CTG TCG GTG GTC ACC TGG AAC AAA	8179
Asn Glu Gly Ser Arg Thr Ala Leu Ser Val Val Thr Trp Asn Lys	
240 245 250	
GAT ATG GTG ACT AGA GTG ACC CCC GAG GGG TCC GAA GAG TGG TCC	8224
Asp Met Val Thr Arg Val Thr Pro Glu Gly Ser Glu Glu Trp Ser	
255 260 265	

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Figure 5 (14)

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GCC CCG CTG ATT ACT GCC ATG TGT GTC CTT GCC AAT GCT ACC TTC	8269
Ala Pro Leu Ile Thr Ala Met Cys Val Leu Ala Asn Ala Thr Phe	
270 275 280	
CCG TGC TTC CAG CCC CCG TGT GTA CCT TGC TGC TAT GAA AAC AAC	8314
Pro Cys Phe Gln Pro Pro Cys Val Pro Cys Cys Tyr Glu Asn Asn	
285 290 295	
GCA GAG GCC ACA CTA CCG ATG CTC GAG GAT AAC GTG GAT AGG CCA	8359
Ala Glu Ala Thr Leu Arg Met Leu Glu Asp Asn Val Asp Arg Pro	
300 305 310	
GGG TAC TAC GAC CTC CTT CAG GCA GCC TTG ACG TGC CGA AAC GGA	8404
Gly Tyr Tyr Asp Leu Leu Gln Ala Ala Leu Thr Cys Arg Asn Gly	
315 320 325	
ACA AGA CAC CCG CGC AGC GTG TCG CAA CAC TTC AAC GTG TAT AAG	8449
Thr Arg His Arg Arg Ser Val Ser Gln His Phe Asn Val Tyr Lys	
330 335 340	
GCT ACA CGC CCT TAC ATC GCG TAC TGC GCC GAC TGC GGA GCA GGG	8494
Ala Thr Arg Pro Tyr Ile Ala Tyr Cys Ala Asp Cys Gly Ala Gly	
345 350 355	
CAC TCG TGT CAT AGC CCC GTA GCA ATT GAA GCG GTC AGG TCC GAA	8539
His Ser Cys His Ser Pro Val Ala Ile Glu Ala Val Arg Ser Glu	
360 365 370	
GCT ACC GAC GGG ATG CTG AAG ATT CAG TTC TCG GCA CAA ATT GCC	8584
Ala Thr Asp Gly Met Leu Lys Ile Gln Phe Ser Ala Gln Ile Gly	
375 380 385	
ATA GAT AAG AGT GAC AAT CAT GAC TAC ACG AAG ATA AGG TAC GCA	8629
Ile Asp Lys Ser Asp Asn His Asp Tyr Thr Lys Ile Arg Tyr Ala	
390 395 400	
GAC GGG CAC GCC ATT GAG AAT GCC GTC CCG TCA TCT TTG AAG GTA	8674
Asp Gly His Ala Ile Glu Asn Ala Val Arg Ser Ser Leu Lys Val	
405 410 415	
GCC ACC TCC GGA GAC TGT TTC GTC CAT GGC ACA ATG GGA CAT TTC	8719
Ala Thr Ser Gly Asp Cys Phe Val His Gly Thr Met Gly His Phe	
420 425 430	
ATA CTG GCA AAG TGC CCA CCG GGT GAA TTC CTG CAG GTC TCG ATC	8764
Ile Leu Ala Lys Cys Pro Pro Gly Glu Phe Leu Gln Val Ser Ile	
435 440 445	
CAG GAC ACC AGA AAC GCG GTC CGT GCC TGC AGA ATA CAA TAT CAT	8809
Gln Asp Thr Arg Asn Ala Val Arg Ala Cys Arg Ile Gln Tyr His	
450 455 460	
CAT GAC CCT CAA CCG GTG GGT AGA GAA AAA TTT ACA ATT AGA CCA	8854
His Asp Pro Gln Pro Val Gly Arg Glu Lys Phe Thr Ile Arg Pro	
465 470 475	

Figure 5 (15)

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CAC	TAT	GGA	AAA	GAG	ATC	CCT	TGC	ACC	ACT	TAT	CAA	CAG	ACC	ACA	8899
His	Tyr	Gly	Lys	Glu	Ile	Pro	Cys	Thr	Thr	Tyr	Gln	Gln	Thr	Thr	
480						485					490				
GCG	AAG	ACC	GTG	GAG	GAA	ATC	GAC	ATG	CAT	ATG	CCG	CCA	GAT	ACG	8944
Ala	Lys	Thr	Val	Glu	Glu	Ile	Asp	Met	His	Met	Pro	Pro	Asp	Thr	
495						500					505				
CCG	GAC	AGG	ACG	TTG	CTA	TCA	CAG	CAA	TCT	GGC	AAT	GTA	AAG	ATC	8989
Pro	Asp	Arg	Thr	Leu	Leu	Ser	Gln	Gln	Ser	Gly	Asn	Val	Lys	Ile	
510						515					520				
ACA	GTC	GGA	GGA	AAG	AAG	GTG	AAA	TAC	AAC	TGC	ACC	TGT	GGA	ACC	9034
Thr	Val	Gly	Gly	Lys	Lys	Val	Lys	Tyr	Asn	Cys	Thr	Cys	Gly	Thr	
525						530					535				
GGA	AAC	GTT	GGC	ACT	ACT	AAT	TCG	GAC	ATG	ACG	ATC	AAC	ACG	TGT	9079
Gly	Asn	Val	Gly	Thr	Thr	Asn	Ser	Asp	Met	Thr	Ile	Asn	Thr	Cys	
540						545					550				
CTA	ATA	GAG	CAG	TGC	CAC	GTC	TCA	GTG	ACG	GAC	CAT	AAG	AAA	TGG	9124
Leu	Ile	Glu	Gln	Cys	His	Val	Ser	Val	Thr	Asp	His	Lys	Lys	Trp	
555						560					565				
CAG	TTC	AAC	TCA	CCT	TTC	GTC	CCG	AGA	GCC	GAC	GAA	CCG	GCT	AGA	9169
Gln	Phe	Asn	Ser	Pro	Phe	Val	Pro	Arg	Ala	Asp	Glu	Pro	Ala	Arg	
570						575					580				
AAA	GGC	AAA	GTC	CAT	ATC	CCA	TTC	CCG	TTG	GAC	AAC	ATC	ACA	TGC	9214
Lys	Gly	Lys	Val	His	Ile	Pro	Phe	Pro	Leu	Asp	Asn	Ile	Thr	Cys	
585						590					595				
AGA	GTT	CCA	ATG	GCG	GCG	GAA	CCA	ACC	GTC	ATC	CAC	GGC	AAA	AGA	9259
Arg	Val	Pro	Met	Ala	Arg	Glu	Pro	Thr	Val	Ile	His	Gly	Lys	Arg	
600						605					610				
GAA	GTG	ACA	CTG	CAC	CTT	CAC	CCA	GAT	CAT	CCC	ACG	CTC	TTT	TCC	9304
Glu	Val	Thr	Leu	His	Leu	His	Pro	Asp	His	Pro	Thr	Leu	Phe	Ser	
615						620					625				
TAC	CGC	ACA	CTG	GGT	GAG	GAC	CCG	CAG	TAT	CAC	GAG	GAA	TGG	GTG	9349
Tyr	Arg	Thr	Leu	Gly	Glu	Asp	Pro	Gln	Tyr	His	Glu	Glu	Trp	Val	
630						635					640				
ACA	GCG	GCG	GTG	GAA	CGG	ACC	ATA	CCC	GTA	CCA	GTG	GAC	GGG	ATG	9394
Thr	Ala	Ala	Val	Glu	Arg	Thr	Ile	Pro	Val	Pro	Val	Asp	Gly	Met	
645						650					655				
GAG	TAC	CAC	TGG	GGA	AAC	AAC	GAC	CCA	GTG	AGG	CTT	TGG	TCT	CAA	9439
Glu	Tyr	His	Trp	Gly	Asn	Asn	Asp	Pro	Val	Arg	Leu	Trp	Ser	Gln	
660						665					670				
CTC	ACC	ACT	GAA	GGG	AAA	CCG	CAC	GGC	TGG	CCG	CAT	CAG	ATC	GTA	9484
Leu	Thr	Thr	Glu	Gly	Lys	Pro	His	Gly	Trp	Pro	His	Gln	Ile	Val	
675						680					685				

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Figure 5 (16)

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CAG TAC TAC TAT GGG CTT TAC CCG GCC GCT ACA GTA TCC GCG GTC	9529
Gln Tyr Tyr Tyr Gly Leu Tyr Pro Ala Ala Thr Val Ser Ala Val	
690 695 700	
GTC GGG ATG AGC TTA CTG GCG TTG ATA TCG ATC TTC GCG TCG TGC	9574
Val Gly Met Ser Leu Leu Ala Leu Ile Ser Ile Phe Ala Ser Cys	
705 710 715	
TAC ATG CTG GTT GCG GCC CGC AGT AAG TGC TTG ACC CCT TAT GCT	9619
Tyr Met Leu Val Ala Ala Arg Ser Lys Cys Leu Thr Pro Tyr Ala	
720 725 730	
TTA ACA CCA GGA GCT GCA GTT CCG TGG ACG CTG GCG ATA CTC TGC	9664
Leu Thr Pro Gly Ala Ala Val Pro Trp Thr Leu Gly Ile Leu Cys	
735 740 745	
TGC GCC CCG CGG GCG CAC GCA GCT AGT GTG GCA GAG ACT ATG GCC	9709
Cys Ala Pro Arg Ala His Ala Ala Ser Val Ala Glu Thr Met Ala	
750 755 760	
TAC TTG TGG GAC CAA AAC CAA GCG TTG TTC TGG TTG GAG TTT GCG	9754
Tyr Leu Trp Asp Gln Asn Gln Ala Leu Phe Trp Leu Glu Phe Ala	
765 770 775	
GCC CCT GTT GCC TGC ATC CTC ATC ATC ACG TAT TGC CTC AGA AAC	9799
Ala Pro Val Ala Cys Ile Leu Ile Ile Thr Tyr Cys Leu Arg Asn	
780 785 790	
GTG CTG TGT TGC TGT AAG AGC CTT TCT TTT TTA GTG CTA CTG AGC	9844
Val Leu Cys Cys Cys Lys Ser Leu Ser Phe Leu Val Leu Leu Ser	
795 800 805	
CTC GGG GCA ACC GCC AGA GCT TAC GAA CAT TCG ACA GTA ATG CCG	9889
Leu Gly Ala Thr Ala Arg Ala Tyr Glu His Ser Thr Val Met Pro	
810 815 820	
AAC GTG GTG GGG TTC CCG TAT AAG GCT CAC ATT GAA AGG CCA GGA	9934
Asn Val Val Gly Phe Pro Tyr Lys Ala His Ile Glu Arg Pro Gly	
825 830 835	
TAT AGC CCC CTC ACT TTG CAG ATG CAG GTT GTT GAA ACC AGC CTC	9979
Tyr Ser Pro Leu Thr Leu Gln Met Gln Val Val Glu Thr Ser Leu	
840 845 850	
GAA CCA ACC CTT AAT TTG GAA TAC ATA ACC TGT GAG TAC AAG ACG	10024
Glu Pro Thr Leu Asn Leu Glu Tyr Ile Thr Cys Glu Tyr Lys Thr	
855 860 865	
GTC GTC CCG TCG CCG TAC GTG AAG TGC TGC GGC GCC TCA GAG TGC	10069
Val Val Pro Ser Pro Tyr Val Lys Cys Cys Gly Ala Ser Glu Cys	
870 875 880	
TCC ACT AAA GAG AAG CCT GAC TAC CAA TGC AAG GTT TAC ACA GGC	10114
Ser Thr Lys Glu Lys Pro Asp Tyr Gln Cys Lys Val Tyr Thr Gly	
885 890 895	



Figure 5 (17)

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GTG TAC CCG TTC ATG TGG GGA GGG GCA TAT TGC TTC TGC GAC TCA	10159
Val Tyr Pro Phe Met Trp Gly Gly Ala Tyr Cys Phe Cys Asp Ser	
900 905 910	
GAA AAC ACG CAA CTC AGC GAG GCG TAC GTC GAT CGA TCG GAC GTA	10204
Glu Asn Thr Gln Leu Ser Glu Ala Tyr Val Asp Arg Ser Asp Val	
915 920 925	
TGC AGG CAT GAT CAC GCA TCT GCT TAC AAA GCC CAT ACA GCA TCG	10249
Cys Arg His Asp His Ala Ser Ala Tyr Lys Ala His Thr Ala Ser	
930 935 940	
CTG AAG GCC AAA GTG AGG GTT ATG TAC GGC AAC GTA AAC CAG ACT	10294
Leu Lys Ala Lys Val Arg Val Met Tyr Gly Asn Val Asn Gln Thr	
945 950 955	
GTG GAT GTT TAC GTG AAC GGA GAC CAT GCC GTC ACG ATA GGG GGT	10339
Val Asp Val Tyr Val Asn Gly Asp His Ala Val Thr Ile Gly Gly	
960 965 970	
ACT CAG TTC ATA TTC GGG CCG CTG TCA TCG GCC TGG ACC CCG TTC	10384
Thr Gln Phe Ile Phe Gly Pro Leu Ser Ser Ala Trp Thr Pro Phe	
975 980 985	
GAC AAC AAG ATA GTC GTG TAC AAA GAC GAA GTG TTC AAT CAG GAC	10429
Asp Asn Lys Ile Val Val Tyr Lys Asp Glu Val Phe Asn Gln Asp	
990 995 1000	
TTC CCG CCG TAC GGA TCT GGG CAA CCA GGG CGC TTC GGC GAC ATC	10474
Phe Pro Pro Tyr Gly Ser Gly Gln Pro Gly Arg Phe Gly Asp Ile	
1005 1010 1015	
CAA AGC AGA ACA GTG GAG AGT AAC GAC CTG TAC GCG AAC ACG GCA	10519
Gln Ser Arg Thr Val Glu Ser Asn Asp Leu Tyr Ala Asn Thr Ala	
1020 1025 1030	
CTG AAG CTG GCA CGC CCT TCA CCC GGC ATG GTC CAT GTA CCG TAC	10564
Leu Lys Leu Ala Arg Pro Ser Pro Gly Met Val His Val Pro Tyr	
1035 1040 1045	
ACA CAG ACA CCT TCA GGG TTC AAA TAT TGG CTA AAG GAA AAA GGG	10609
Thr Gln Thr Pro Ser Gly Phe Lys Tyr Trp Leu Lys Glu Lys Gly	
1050 1055 1060	
ACA GCC CTA AAT ACG AAG GCT CCT TTT GGC TGC CAA ATC AAA ACG	10654
Thr Ala Leu Asn Thr Lys Ala Pro Phe Gly Cys Gln Ile Lys Thr	
1065 1070 1075	
AAC CCT GTC AGG GCC ATG AAC TGC GCC GTG GGA AAC ATC CCT GTC	10699
Asn Pro Val Arg Ala Met Asn Cys Ala Val Gly Asn Ile Pro Val	
1080 1085 1090	
TCC ATG AAT TTG CCT GAC AGC GCC TTT ACC CGC ATT GTC GAG GCG	10744
Ser Met Asn Leu Pro Asp Ser Ala Phe Thr Arg Ile Val Glu Ala	
1095 1100 1105	

Figure 5 (18)

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CCG ACC ATC ATT GAC CTG ACT TGC ACA GTG GCT ACC TGT ACG CAC 10789  
 Pro Thr Ile Ile Asp Leu Thr Cys Thr Val Ala Thr Cys Thr His  
 1110 1115 1120

TCC TCG GAT TTC GGC GGC GTC TTG ACA CTG ACG TAC AAG ACC AAC 10834  
 Ser Ser Asp Phe Gly Gly Val Leu Thr Leu Thr Tyr Lys Thr Asn  
 1125 1130 1135

AAG AAC GGG GAC TGC TCT GTA CAC TCG CAC TCT AAC GTA GCT ACT 10879  
 Lys Asn Gly Asp Cys Ser Val His Ser His Ser Asn Val Ala Thr  
 1140 1145 1150

CTA CAG GAG GCC ACA GCA AAA GTG AAG ACA GCA GGT AAG GTG ACC 10924  
 Leu Gln Glu Ala Thr Ala Lys Val Lys Thr Ala Gly Lys Val Thr  
 1155 1160 1165

TTA CAC TTC TCC ACG GCA AGC GCA TCA CCT TCT TTT GTG GTG TCG 10969  
 Leu His Phe Ser Thr Ala Ser Ala Ser Pro Ser Phe Val Val Ser  
 1170 1175 1180

CTA TGC AGT GCT AGG GCC ACC TGT TCA GCG TCG TGT GAG CCC CCG 11014  
 Leu Cys Ser Ala Arg Ala Thr Cys Ser Ala Ser Cys Glu Pro Pro  
 1185 1190 1195

AAA GAC CAC ATA GTC CCA TAT GCG GCT AGC CAC AGT AAC GTA GTG 11059  
 Lys Asp His Ile Val Pro Tyr Ala Ala Ser His Ser Asn Val Val  
 1200 1205 1210

TTT CCA GAC ATG TCG GGC ACC GCA CTA TCA TGG GTG CAG AAA ATC 11104  
 Phe Pro Asp Met Ser Gly Thr Ala Leu Ser Trp Val Gln Lys Ile  
 1215 1220 1225

TCG GGT GGT CTG GGC GCC TTC GCA ATC GGC GCT ATC CTG GTG CTG 11149  
 Ser Gly Gly Leu Gly Ala Phe Ala Ile Gly Ala Ile Leu Val Leu  
 1230 1235 1240

GTT GTG GTC ACT TGC ATT GGG CTC CGC AGA TAA GTTAGGGTAG 11192  
 Val Val Val Thr Cys Ile Gly Leu Arg Arg  
 1245 1250

GCAATGGCAT TGATATAGCA AGAAAATTGA AAACAGAAAA AGTTAGGGTA AGCAATGGCA 11252

TATAACCATA ACTGTATAAC TTGTAACAAA GCGCAACAAG ACCTGCGCAA TTGGCCCCGT 11312

GGTCCGCCTC ACGGAAACTC GGGGCAACTC ATATTGACAC ATTAATTGGC AATAATTGGA 11372

AGCTTACATA AGCTTAATTC GACGAATAAT TGGATTTTTA TTTTATTTTG CAATTGGTTT 11432

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AAAAAAAAAA AAAAAAAAAA ACTAG 11517

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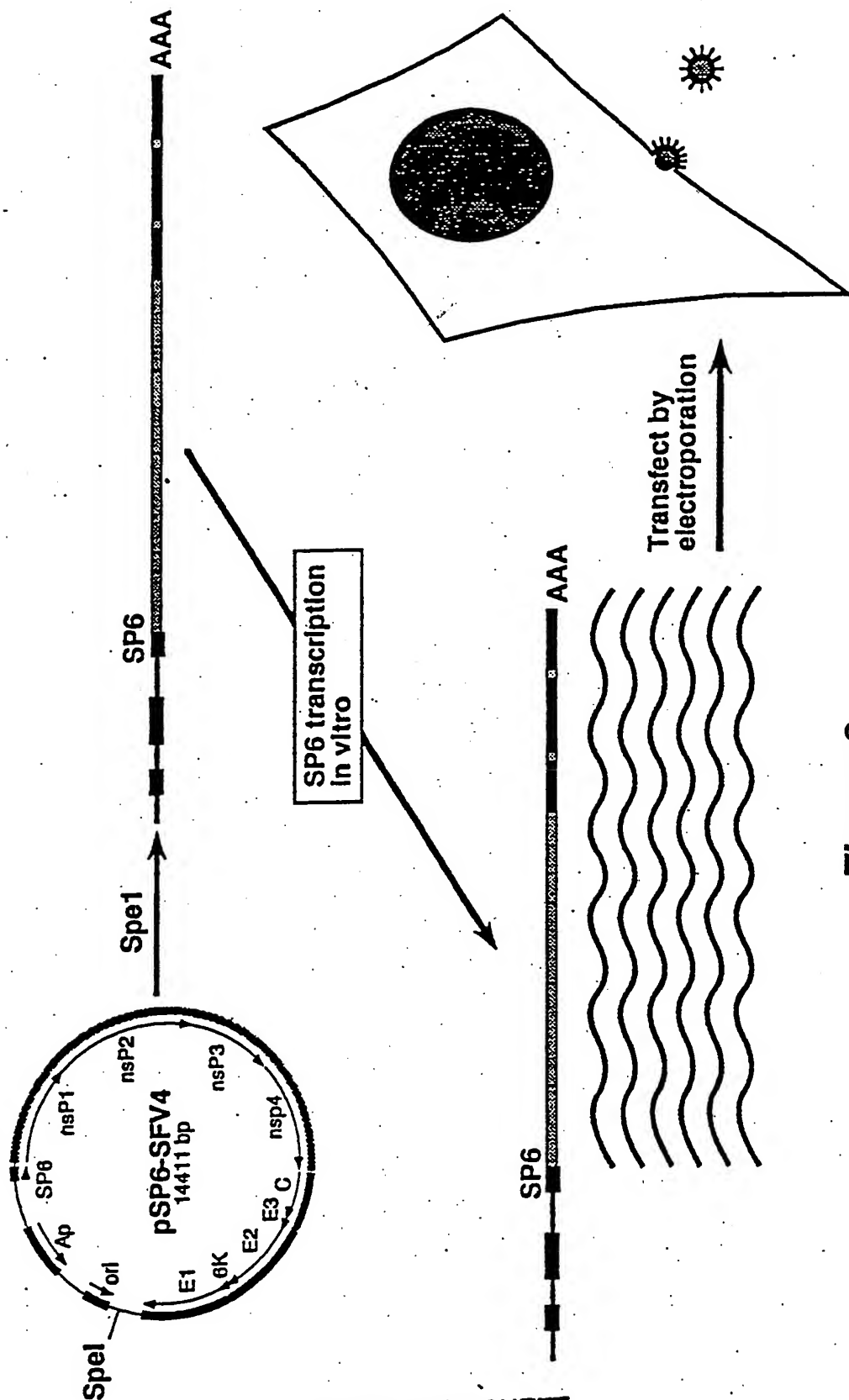


Figure 6

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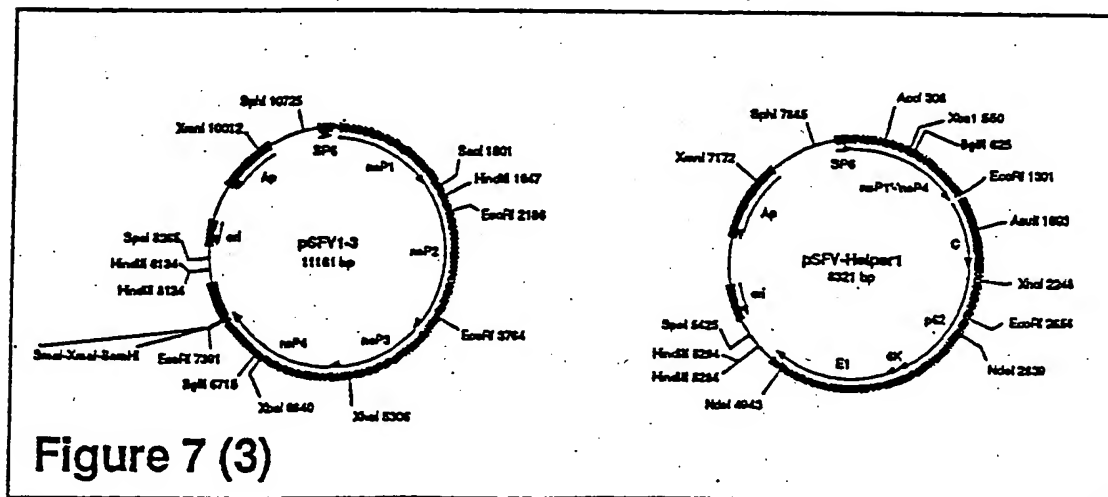
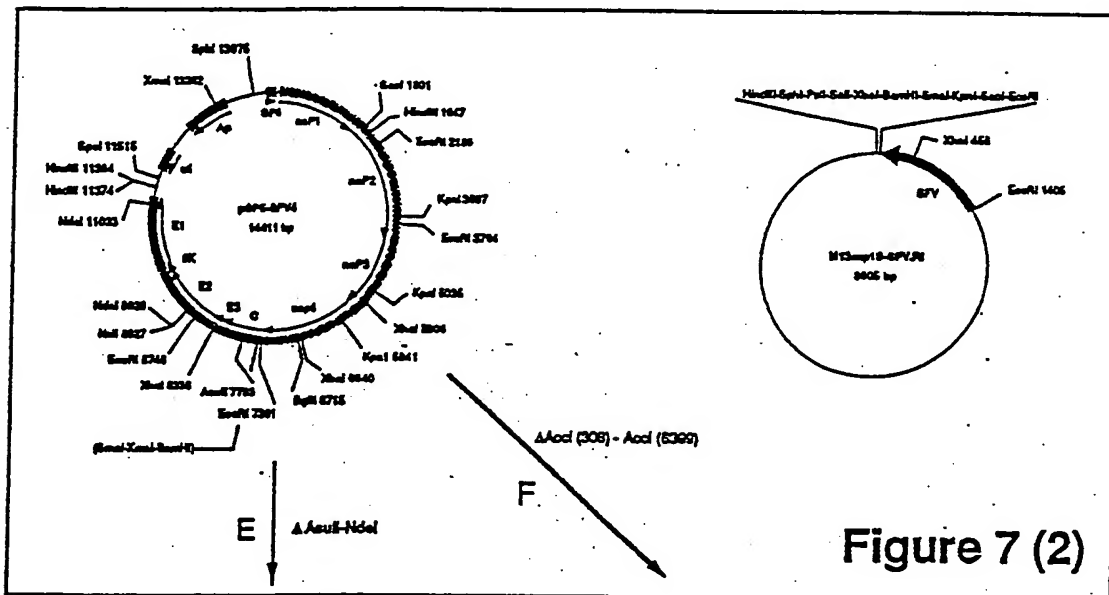
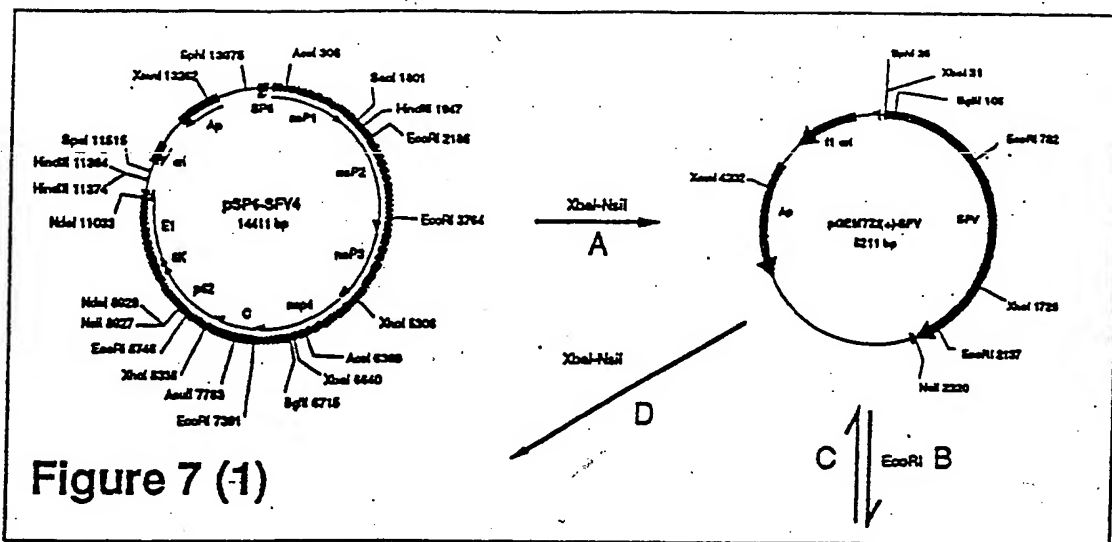


Figure 7 layout scheme

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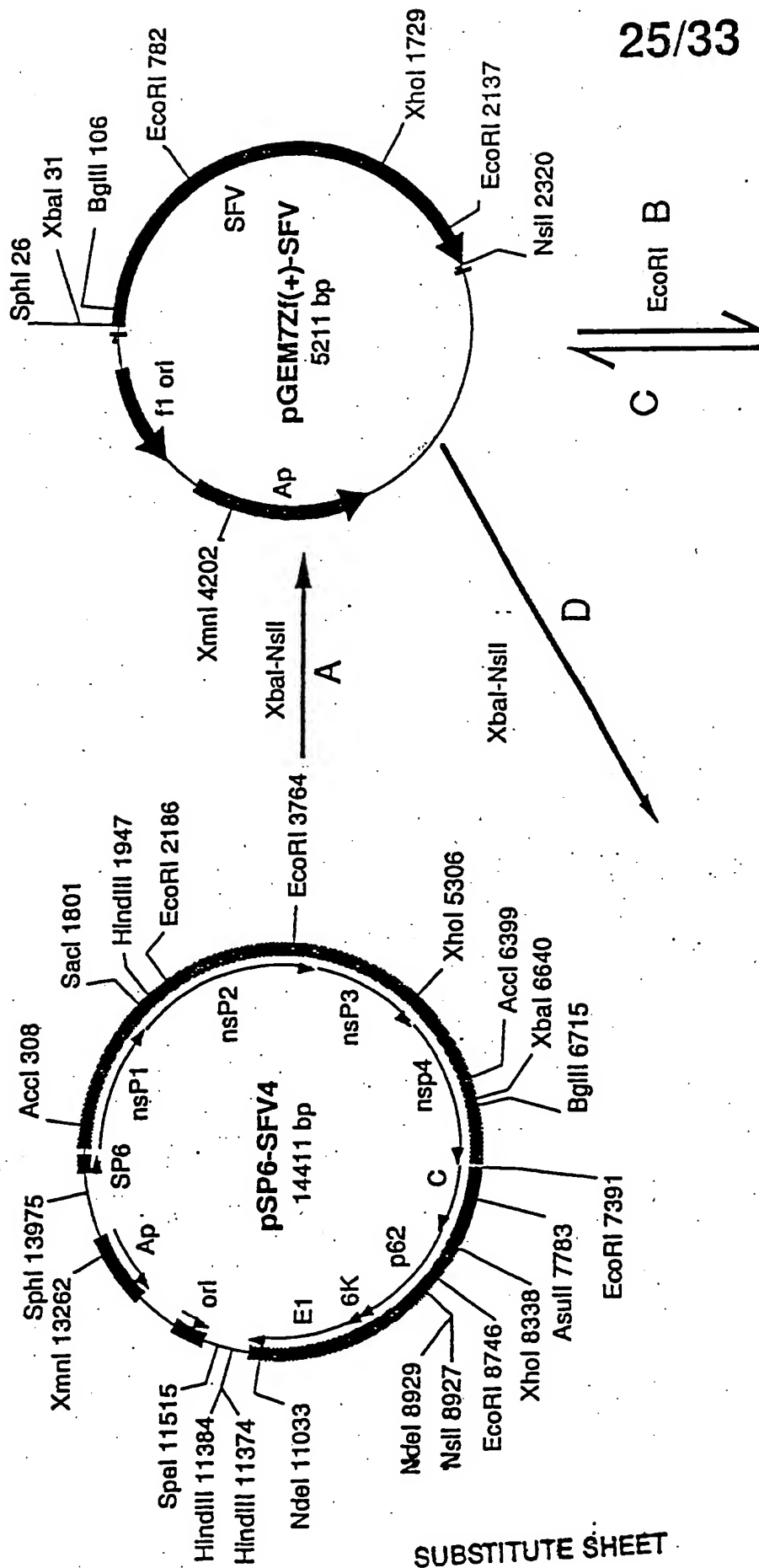


Figure 7 (1)

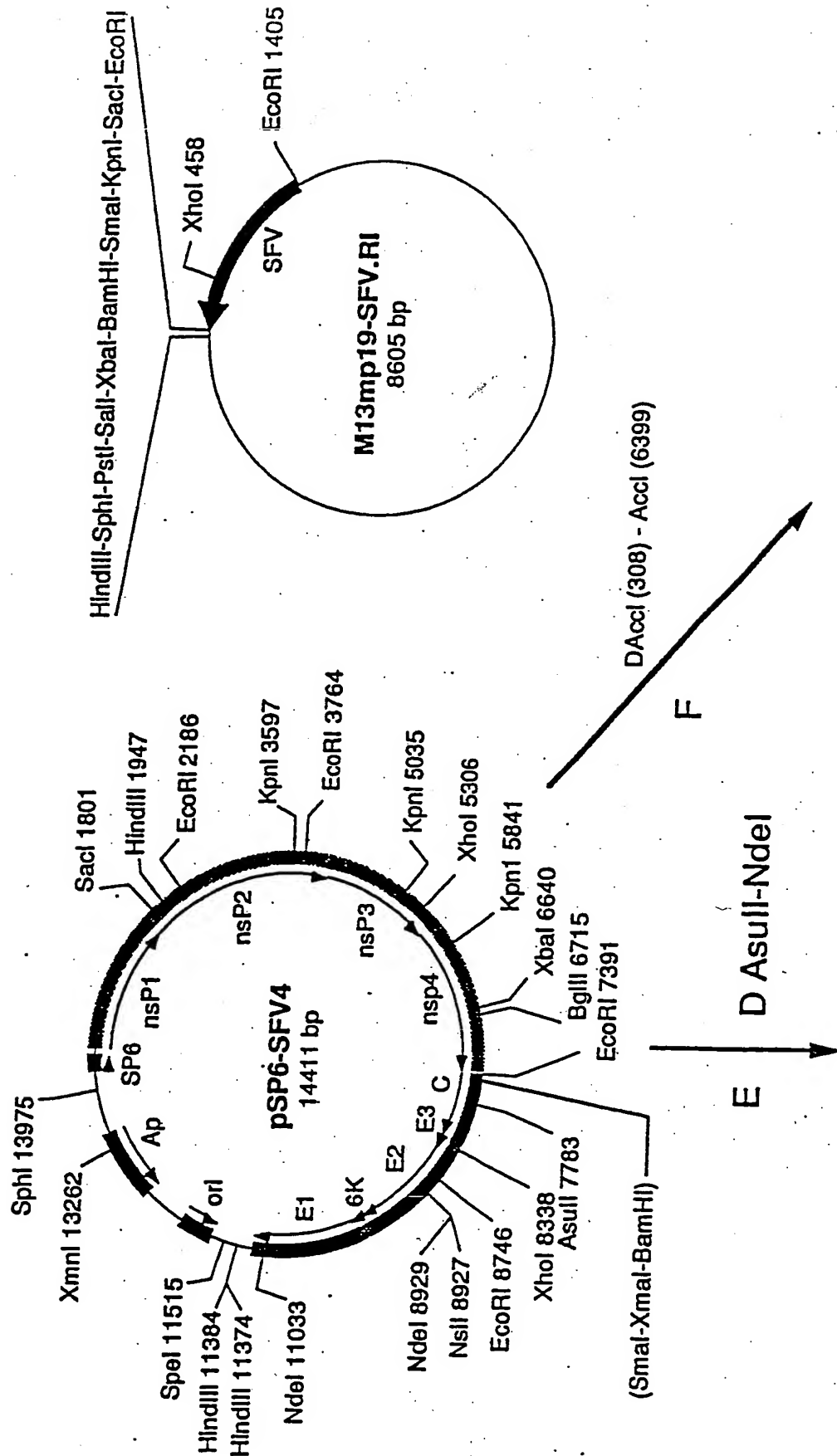


Figure 7 (2)

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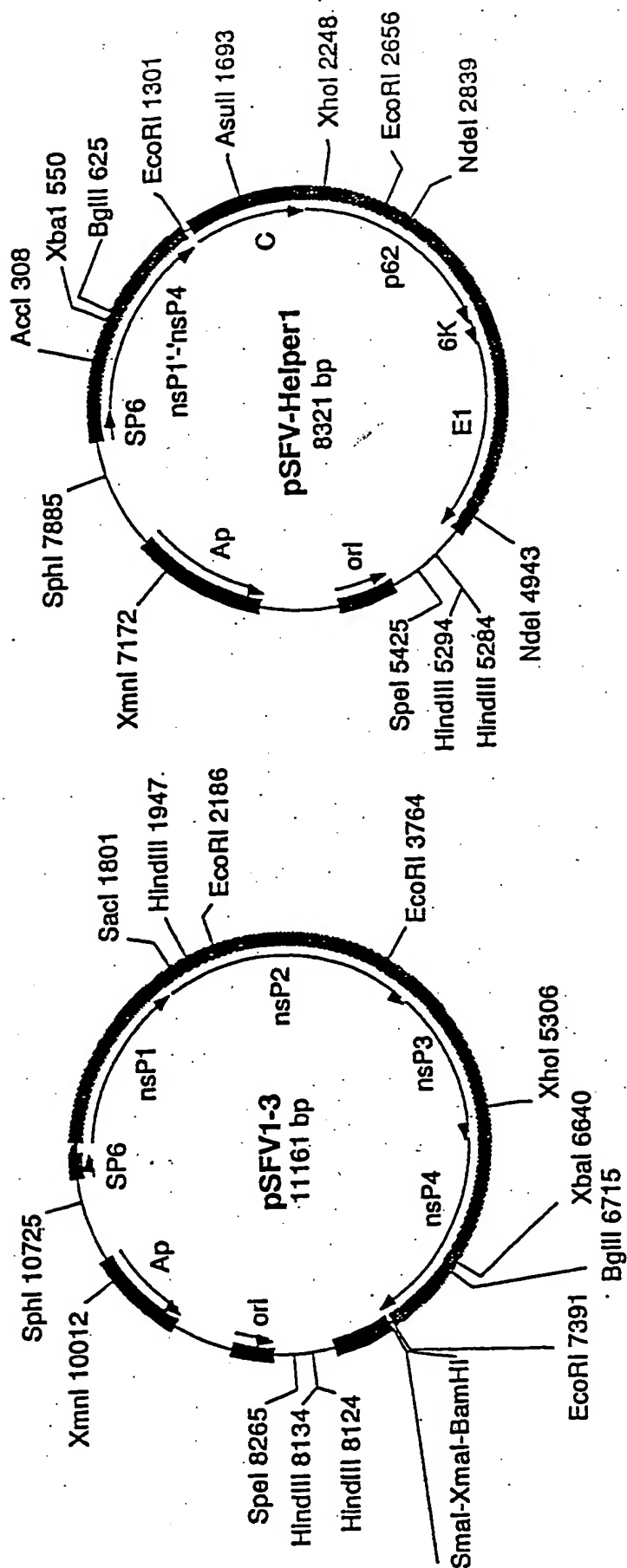
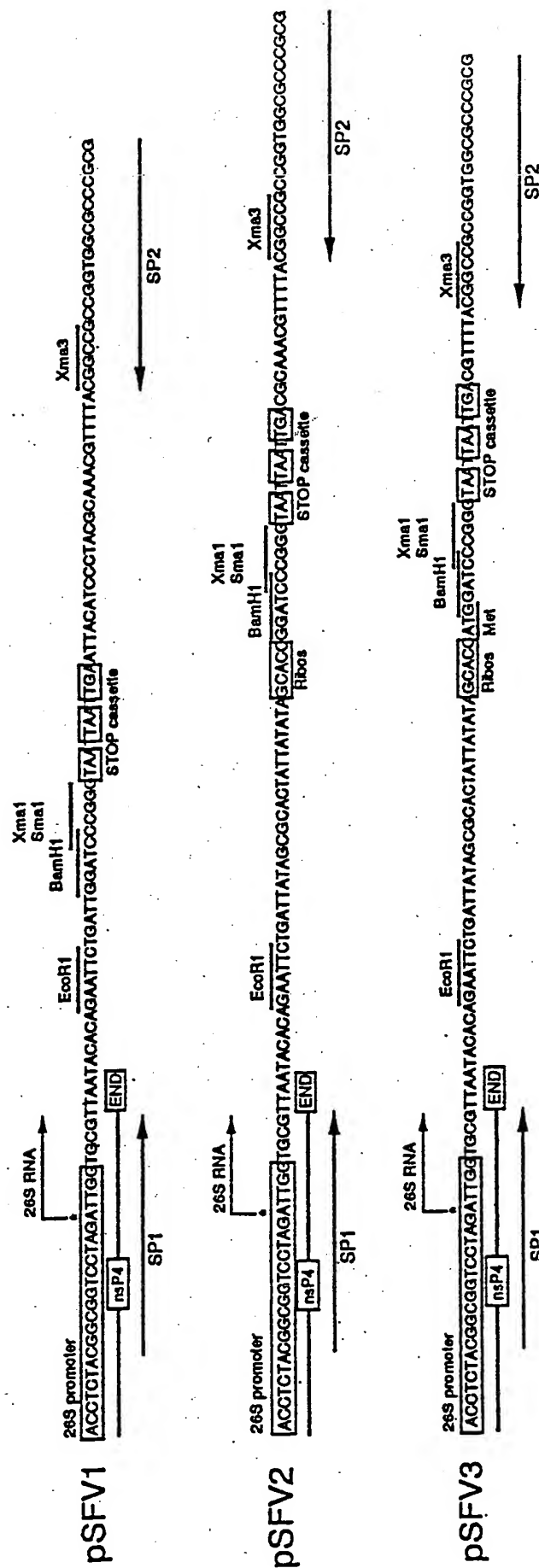
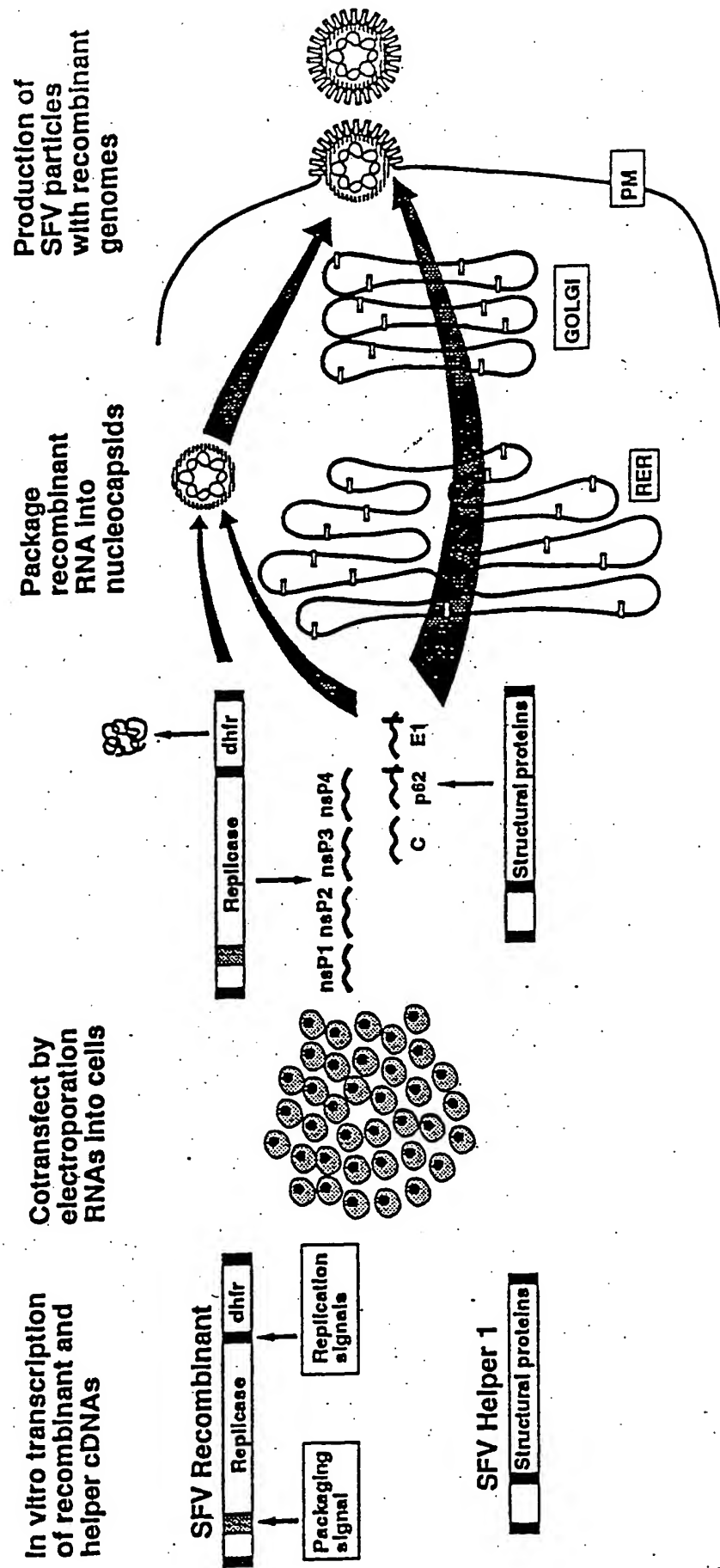


Figure 7 (3)







### Figure 9

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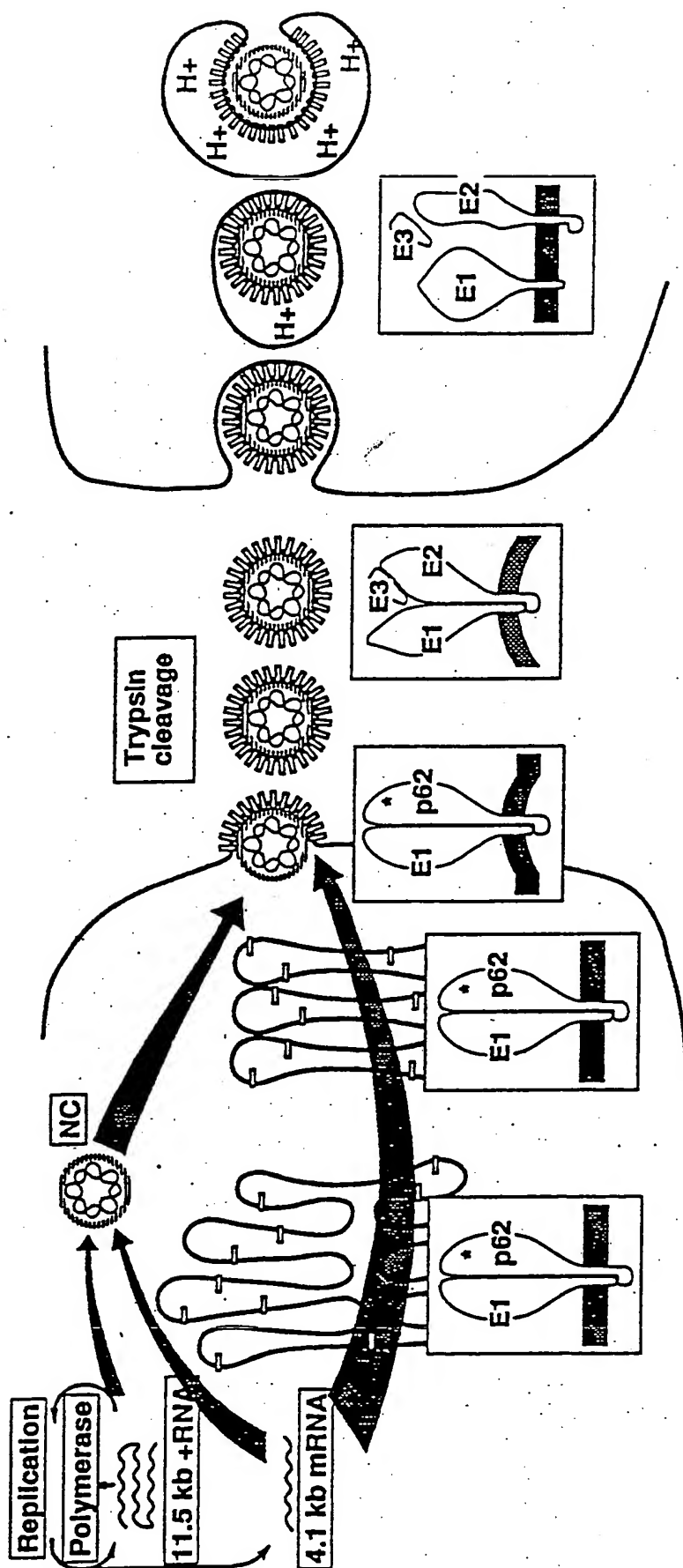


Figure 10

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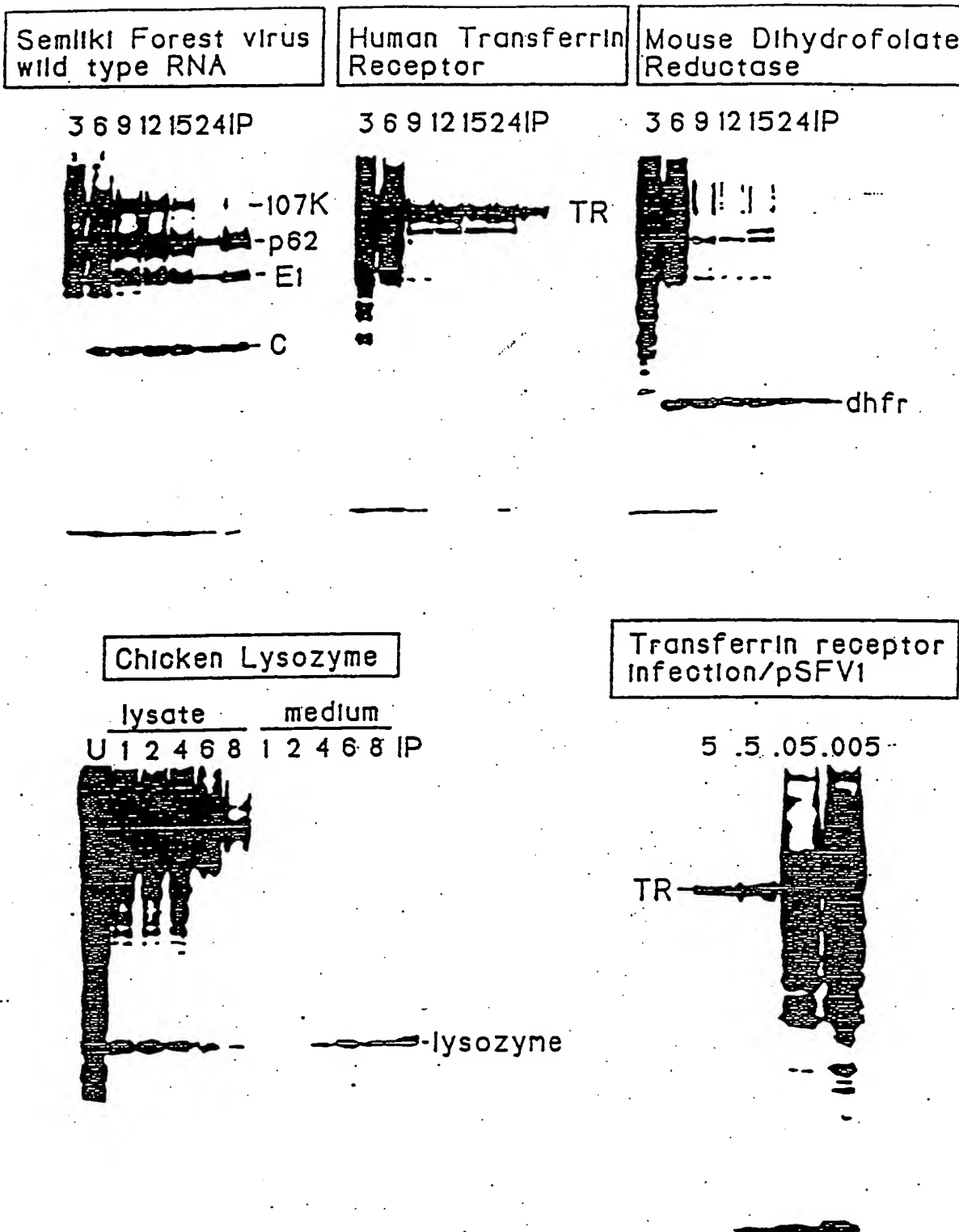


Figure 11

SUBSTITUTE SHEET

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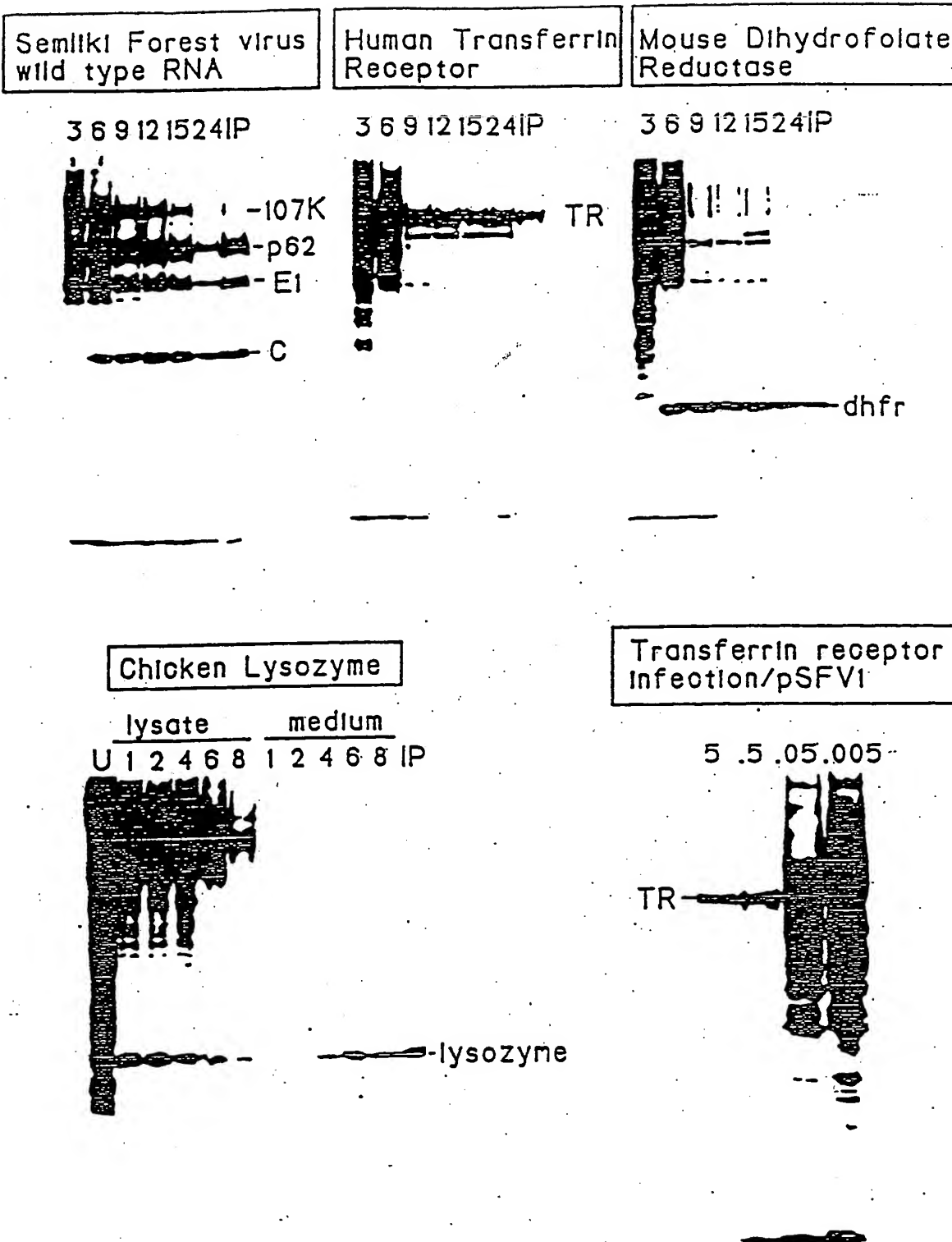
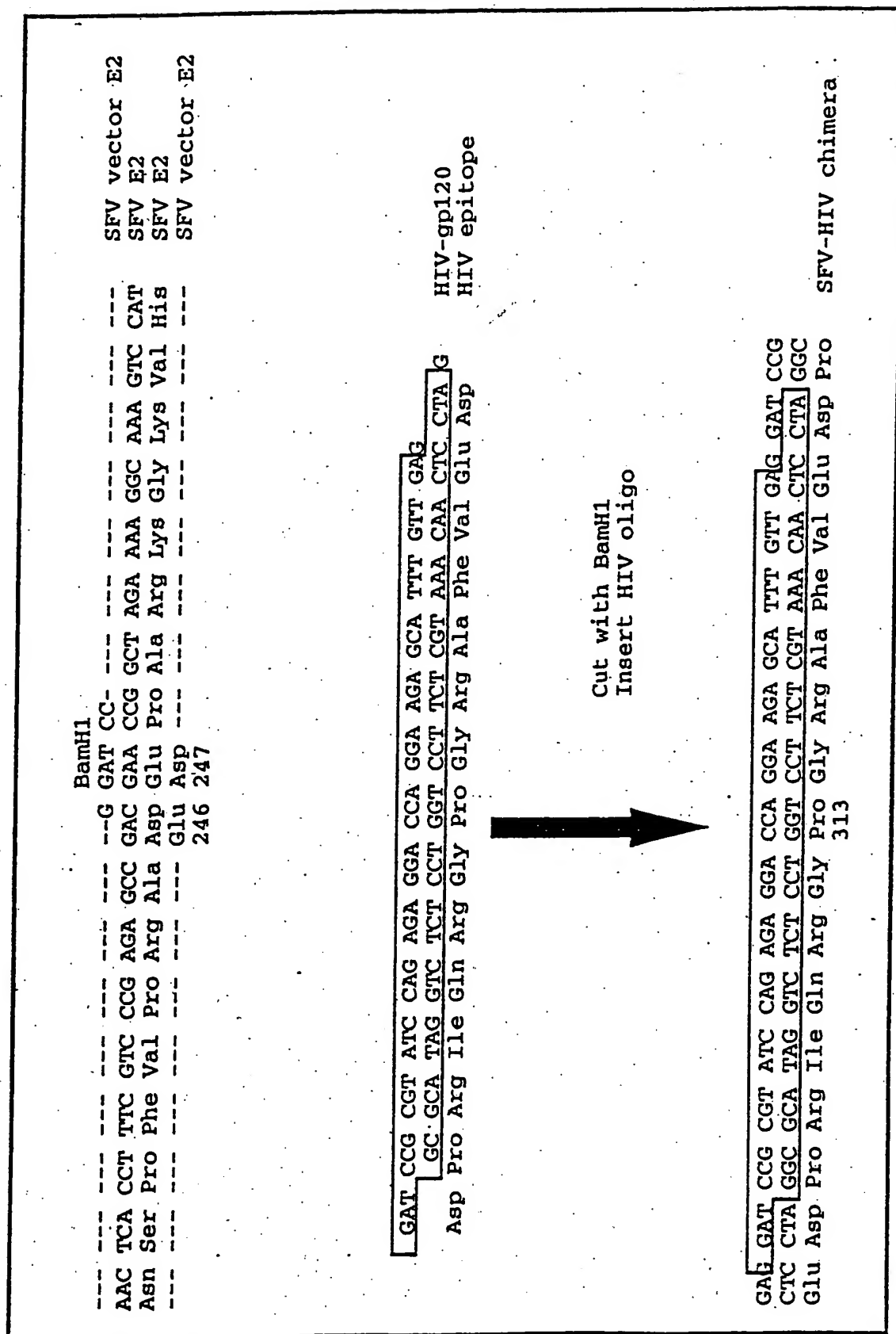


Figure 11

SUBSTITUTE SHEET

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### Figure 12 (1)

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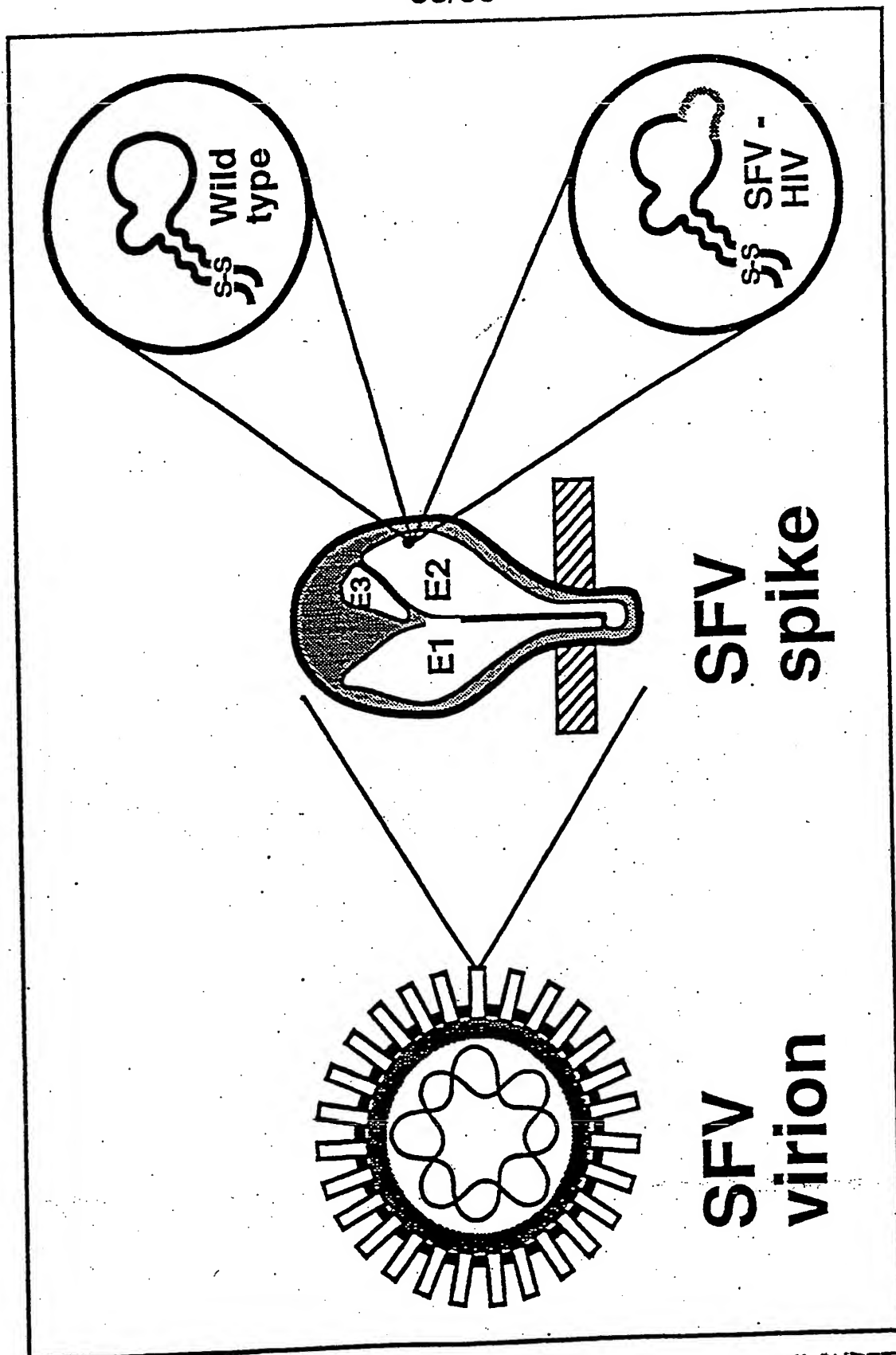


Figure 12 (2)

# INTERNATIONAL SEARCH REPORT

International Application No. PCT/SE 91/00855

<b>I. CLASSIFICATION OF SUBJECT MATTER</b> (If several classification symbols apply, indicate all) <sup>6</sup> According to International Patent Classification (IPC) or to both National Classification and IPC IPC5: C 12 N 15/86, C 12 N 7/01, A 61 K 39/12		
<b>II. FIELDS SEARCHED</b> <div style="text-align: center;">Minimum Documentation Searched<sup>7</sup></div>		
Classification System	Classification Symbols	
IPC5	C 12 N; A 61 K	
Documentation Searched other than Minimum Documentation to the extent that such Documents are included in Fields Searched <sup>8</sup>		
SE,DK,FI,NO classes as above		
<b>III. DOCUMENTS CONSIDERED TO BE RELEVANT<sup>9</sup></b>		
Category *	Citation of Document, <sup>11</sup> with indication, where appropriate, of the relevant passages <sup>12</sup>	Relevant to Claim No. <sup>13</sup>
X	PROC.NATL.ACAD.SCI., Vol. 84, 1987 (USA) Robin Levis et al: "Engineered defective interfering RNAs of Sindbis virus express bacterial chloramphenicol acetyltransferase in avian cells", see page 4811 - page 4815 especially page 4811, column 1 lines 1-4,12-15,46-48; column 2 lines 25-28 and page 4812 column 1 lines 24-26 column 2 lines 14-16	1-2,5,9-11,20-22,29,30
Y		3,4,6-8,12-19,23-28,31-41
Y	WO, A1, 8912095 (APPLIED BIOTECHNOLOGY, INC.) 14 December 1989, see the whole document	3,4,6-8,12-19,23-28,31-41
<div style="display: flex; justify-content: space-between;"> <div style="width: 45%;"> <p>* Special categories of cited documents:<sup>10</sup></p> <p>"A" document defining the general state of the art which is not considered to be of particular relevance</p> <p>"E" earlier document but published on or after the international filing date</p> <p>"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)</p> <p>"O" document referring to an oral disclosure, use, exhibition or other means</p> <p>"P" document published prior to the international filing date but later than the priority date claimed</p> </div> <div style="width: 45%;"> <p>"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention</p> <p>"X" document of particular relevance, the claimed invention cannot be considered novel or cannot be considered to involve an inventive step</p> <p>"Y" document of particular relevance, the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art</p> <p>"Z" document member of the same patent family</p> </div> </div>		
<b>IV. CERTIFICATION</b>		
Date of the Actual Completion of the International Search	Date of Mailing of this International Search Report	
17th March 1992	1992 -03- 19	
International Searching Authority	Signature of Authorized Officer	
SWEDISH PATENT OFFICE	<i>Carolina Palmcrantz</i> Carolina Palmcrantz	

III. DOCUMENTS CONSIDERED TO BE RELEVANT (CONTINUED FROM THE SECOND SHEET)		Relevant to Claim No.
Category	Citation of Document, with indication, where appropriate, of the relevant passages	
X	<p>Dialog Information Services, file 154, MEDLINE 85-91/July, Dialog accession no. 06757425, Medline accession no. 89059425, "Alphaviruses a new vector expressing heterologous genes", Vopr Virusol Jul-Aug 1988, 33 (4) p 502-4</p>	1-2



ANNEX TO THE INTERNATIONAL SEARCH REPORT  
ON INTERNATIONAL PATENT APPLICATION NO. PCT/SE 91/00855

This annex lists the patent family members relating to the patent documents cited in the above-mentioned international search report.  
The members are as contained in the Swedish Patent Office EDP file on 28/02/92  
The Swedish Patent Office is in no way liable for these particulars which are merely given for the purpose of information.

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO-A1- 8912095	89-12-14	AU-D- 3775789	90-01-05

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